

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 13, 2005, 07:46:47 ; Search time 43 Seconds
(without alignments)
539.904 Million cell updates/sec

Title: US-09-263-689-4
Perfect score: 311
Sequence: 1 MAFSGSQAPYLSPAVPFSGT.....LPTINRLEVGDIQLTHVQT 311

Scoring table: OIIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	311	100.0	311	3	US-08-946-914-4
2	311	100.0	311	4	US-09-656-450-4
3	163	52.4	355	4	US-09-326-402C-18
4	163	52.4	378	4	US-09-854-133-439
5	148	47.6	168	4	US-09-401-064-199
6	148	47.6	301	4	US-09-559-023-4
7	87	28.0	323	4	US-09-326-402C-19
8	69	22.2	145	2	US-08-788-584-1
9	69	22.2	149	2	US-08-788-584-3
10	22	7.1	322	4	US-09-559-023-2
11	20	6.4	145	2	US-08-788-584-5
12	20	6.4	145	3	US-08-946-914-12
13	20	6.4	145	4	US-09-656-450-12
14	20	6.4	145	4	US-09-557-170A-3
15	12	3.9	262	3	US-08-946-914-14
16	12	3.9	262	4	US-09-656-450-14
17	10	3.2	275	4	US-09-557-170A-25
18	10	3.2	296	4	US-09-557-170A-27
19	10	3.2	324	3	US-08-946-914-11
20	10	3.2	324	4	US-08-656-450-11
21	10	3.2	336	3	US-09-131-648-1
22	9	2.9	422	4	US-09-270-767-42572
23	8	2.6	43	4	US-08-875-553D-43
24	8	2.6	45	4	US-08-875-553D-41
25	8	2.6	45	4	US-08-875-553D-41
26	8	2.6	46	4	US-08-875-553D-42
27	8	2.6	143	4	US-09-877-790-1

28	8	2.6	200	3	US-08-946-914-8	Sequence 8, Appli
29	8	2.6	200	4	US-09-656-450-8	Sequence 8, Appli
30	8	2.6	249	4	US-09-538-092-951	Sequence 951, App
31	8	2.6	250	1	US-08-562-311-2	Sequence 2, Appli
32	8	2.6	250	3	US-08-946-914-10	Sequence 10, Appli
33	8	2.6	250	4	US-09-656-450-10	Sequence 10, Appli
34	8	2.6	250	4	US-09-919-039-298	Sequence 298, App
35	8	2.6	250	4	US-09-877-790-2	Sequence 2, Appli
36	8	2.6	251	4	US-09-949-016-7560	Sequence 7560, Ap
37	8	2.6	264	1	US-08-562-311-4	Sequence 4, Appli
38	8	2.6	264	2	US-08-728-521-1	Sequence 1, Appli
39	8	2.6	264	3	US-09-212-146-1	Sequence 1, Appli
40	8	2.6	315	4	US-09-326-402C-17	Sequence 17, Appli
41	8	2.6	316	2	US-08-728-521-3	Sequence 3, Appli
42	8	2.6	316	2	US-08-647-960-2	Sequence 2, Appli
43	8	2.6	316	3	US-08-946-914-15	Sequence 15, Appli
44	8	2.6	316	3	US-08-946-914-17	Sequence 17, Appli
45	8	2.6	316	3	US-09-131-648-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-946-914-4
; Sequence 4, Application US/08946914
; Patent No. 6027916
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kassler, Goldstein, & Fox P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,914
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,093
; FILING DATE: 09-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0560001/EKS/SGW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 311 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-946-914-4

Query Match 100.0%; Score 311; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 9.2e-300;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAFSGSQAPYLSPAVPFSGTIOGGLQITVNGTVLSSSGTFANVNFQFGSGNDIAF 60
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Db 1 MAFSGSQAPYLSPAVPFSGTIOGGLQDGLQITVNGTVLSSSGTRFAVNFQTGSGNDIAF 60
Qy 61 HFNPRFDDGGVVCNTRQNSWGPEERKTHMPQKGMPPDLCTLVQSSDFKVMVNGILFV 120
Db 61 HFNPRFDDGGVVCNTRQNSWGPEERKTHMPQKGMPPDLCTLVQSSDFKVMVNGILFV 120
Qy 121 QYFHRVPEFHRVDITISVNGSVQLSIVISFQOTQVHTVQSAQGMFSTPAIPPMYPHPAYP 180
Db 121 QYFHRVPEFHRVDITISVNGSVQLSIVISFQOTQVHTVQSAQGMFSTPAIPPMYPHPAYP 180
Qy 181 MPFITTLGLGYPSKILLSGTVLPSAQRFHNLCSGNHIAFHLNPRFDENAVVRNTQID 240
Db 181 MPFITTLGLGYPSKILLSGTVLPSAQRFHNLCSGNHIAFHLNPRFDENAVVRNTQID 240
Qy 241 NSWGSEERSLPRKMPFVRGQSFVWILCEAHCLKVAVDGQHLFEYHRLNLPINRLEV 300
Db 241 NSWGSEERSLPRKMPFVRGQSFVWILCEAHCLKVAVDGQHLFEYHRLNLPINRLEV 300
Qy 301 GGDQLTHVQT 311
Db 301 GGDQLTHVQT 311

RESULT 2
US-09-656-450-4
; Sequence 4, Application US/09656450
; Patent No. 6468768
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Galectin 9 and 10SV Polynucleotides
; FILE REFERENCE: 1488.0560003
; CURRENT APPLICATION NUMBER: US/09/656,450
; CURRENT FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/263,689
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: US 08/946,914
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: US 60/028,093
; PRIOR FILING DATE: 1996-10-09
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-656-450-4

Query Match 100.0%; Score 311; DB 4; Length 311;
Best Local Similarity 100.0%; Pred. No. 9.2e-300; Mismatches 0; Indels 0; Gaps 0;
Matches 311; Conservative 0;
Qy 1 MAFSGSQAPYLSPAVPFSGTIOGGLQDGLQITVNGTVLSSSGTRFAVNFQTGSGNDIAF 60
Db 1 MAFSGSQAPYLSPAVPFSGTIOGGLQDGLQITVNGTVLSSSGTRFAVNFQTGSGNDIAF 60
Qy 61 HFNPRFDDGGVVCNTRQNSWGPEERKTHMPQKGMPPDLCTLVQSSDFKVMVNGILFV 120
Db 61 HFNPRFDDGGVVCNTRQNSWGPEERKTHMPQKGMPPDLCTLVQSSDFKVMVNGILFV 120
Qy 121 QYFHRVPEFHRVDITISVNGSVQLSIVISFQOTQVHTVQSAQGMFSTPAIPPMYPHPAYP 180
Db 121 QYFHRVPEFHRVDITISVNGSVQLSIVISFQOTQVHTVQSAQGMFSTPAIPPMYPHPAYP 180
Qy 181 MPFITTLGLGYPSKILLSGTVLPSAQRFHNLCSGNHIAFHLNPRFDENAVVRNTQID 240
Db 181 MPFITTLGLGYPSKILLSGTVLPSAQRFHNLCSGNHIAFHLNPRFDENAVVRNTQID 240
Qy 241 NSWGSEERSLPRKMPFVRGQSFVWILCEAHCLKVAVDGQHLFEYHRLNLPINRLEV 300
Db 241 NSWGSEERSLPRKMPFVRGQSFVWILCEAHCLKVAVDGQHLFEYHRLNLPINRLEV 300

Qy 301 GGDQLTHVQT 311
Db 301 GGDQLTHVQT 311
RESULT 3
US-09-326-402C-18
; Sequence 18, Application US/09326402C
; Patent No. 6759192
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Polymorphic Markers of Prostate Carcinoma Tumor Antigen-1 (PCTA-1)
; FILE REFERENCE: GEN-T112XCI
; CURRENT APPLICATION NUMBER: US/09/326,402C
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,187
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/102,324
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(355)
; OTHER INFORMATION: amino acid sequence of gal9-1
US-09-326-402C-18

Query Match 52.4%; Score 163; DB 4; Length 355;
Best Local Similarity 100.0%; Pred. No. 3.9e-153; Mismatches 0; Indels 0; Gaps 0;
Matches 163; Conservative 0;
Qy 149 TQTVIHTVQSAQGMFSTPAIPPMYPHPAYPMPFITTLGGLYPSKILLSGTVLPSAQ 208
Db 193 TQTVIHTVQSAQGMFSTPAIPPMYPHPAYPMPFITTLGGLYPSKILLSGTVLPSAQ 252
Qy 209 RFHNLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFVWILC 268
Db 253 RFHNLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFVWILC 312
Qy 269 EAHCLKVAVDGQHLFEYHRLNLPINRLEVGGDIQLTHVQT 311
Db 313 EAHCLKVAVDGQHLFEYHRLNLPINRLEVGGDIQLTHVQT 355

RESULT 4
US-09-854-133-439
; Sequence 439, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raedoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 439
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-133-439

Query Match	52.4%	Score 163	DB 4	Length 378	
Best Local Similarity	100.0%	Pred. No. 4.2e-153			
Matches 163	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
149	TQTVHTVQSAPGQMFSTPAIPMMYPHPAYPMPFITIILGGLYPSKSIILSGTVLPSAQ	208			
216	TQTVHTVQSAPGQMFSTPAIPMMYPHPAYPMPFITIILGGLYPSKSIILSGTVLPSAQ	275			
209	RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSMGSEERSLPRKMPVPRGQSFVWLIC	268			
276	RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSMGSEERSLPRKMPVPRGQSFVWLIC	335			
269	EAHCLKVAVDGOHLPFYHYHRLRNLPITNRLRVGGDIQLTHVQT	311			
336	EAHCLKVAVDGOHLPFYHYHRLRNLPITNRLRVGGDIQLTHVQT	378			

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RESULT 5
US-09-401-064-199
; Sequence 199, Application US/09401064
; Patent No. 6623923
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; METHOD OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCES: 210121.471C2
; CURRENT APPLICATION NUMBER: US/09/401,064
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 199
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-401-064-199

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	Query Match	47.6%	Score 148;	DB 4;	Length 168;
	Best Local Similarity	100.0%;	Prod. No. 1.4e-138;		
	Matches 148;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAFGSGOAPYLSPAVPESGTTQGGLOGLQITVNGTGLSSSGTSPANNFQFGSGNDIAF	60		
Db	7	MAFGSGOAPYLSPAVPESGTTQGGLOGLQITVNGTGLSSSGTSPANNFQFGSGNDIAF	66		
Qy	61	HFNPRPFDGGVVCNTQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDKFVWNGILFV	120		
Db	67	HFNPRPFDGGVVCNTQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDKFVWNGILFV	126		
Qy	121	QYHRVPFHRVDTISVNGSVQLSVISFQ	148		
Db	127	QYHRVPFHRVDTISVNGSVQLSVISFO	154		

RESULT 6
US-09-559-023--4
; Sequence 4, Application US/09559023
; Patent No. 6551796
; GENERAL INFORMATION:
; APPLICANT: Abramson, Ruth
; APPLICANT: Leal-Pinto, Edgar
; APPLICANT: Lipkowitz, Michael
; TITLE OF INVENTION: NUCLEIC ACID ENCODING URATE TRANSPORTER
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 070165.0574
; CURRENT APPLICATION NUMBER: US/09/559,023
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/221,898

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; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/099,752
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/070,215
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 301
; TYPE: prt
; ORGANISM: Human
US-09-559-023-4

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Query Match	47.6%	Score 148;	DB 4;	Length 301;
Best Local Similarity	100.0%;	Pred. No. 2.4e-138;		
Matches 148;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAPSGSQAPYLSPAVPFSGTIQGGLODGLQITVNGTVLSSSGTRFPAVNFOTGPGSNDIAF	60	
Db	1	MAPSGSQAPYLSPAVPFSGTIQGGLODGLQITVNGTVLSSSGTRFPAVNFOTGPGSNDIAF	60	
Qy	61	HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPPDLCFLVQSSDFKVMVNGILFV	120	
Db	61	HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPPDLCFLVQSSDFKVMVNGILFV	120	
Qy	121	QYHRVPFHRVDITISVNGSVOLSYISFQ	148	
Db	121	QYHRVPFHRVDITISVNGSVOLSYISFQ	148	

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RESULT 7
US-09-326-402C-19
; Sequence 19, Application US/09326402C
; Patent No. 6759192
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Polymorphic Markers of Protein
; FILE REFERENCE: GEN-T112XC1
; CURRENT APPLICATION NUMBER: US/09/326,402C
; CURRENT FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: 60/088,187
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/102,324
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(323)
; OTHER INFORMATION: amino acid sequence of gal
; US-09-326-402C-19

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Query Match	28.0%; Score 87; DB 4; Length 323;
Best Local Similarity	100.0%; Pred. No. 6.6e-78;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MAPSGSQAPYLSPAVPFSGTIOGQLDGLQITVNGTVLSSSGRFAVNFQTGSGNDIAF 60
Dd	1 MAPSGSQAPYLSPAVPFSGTIOGQLDGLQITVNGTVLSSSGRFAVNFQTGSGNDIAF 60
Qy	61 HFNPRFEDGGYVCNTRONGSWGPEER 87
Dd	61 HFNPRFEDGGYVCNTRONGSWGPEER 87

RESULT 8
US-08-788-584-1

```
; Sequence 1, Application US/08788584
; Patent No. 5837493
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Petithory, Joanne R.
; TITLE OF INVENTION: NOVEL HUMAN GALECTINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,584
; FILING DATE: Filed Herewith
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0192 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-788-584-3

Query Match 22.2%; Score 69; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 2.1e-60;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 243 WGSERSLPRKMPFVRGQSFVWLCEAHCLKVAVDQGHLYFYHRLRLPTINRLEVGG 302
Db 81 WGSERSLPRKMPFVRGQSFVWLCEAHCLKVAVDQGHLYFYHRLRLPTINRLEVGG 140

Qy 303 DIQLTHVQT 311
Db 141 DIQLTHVQT 149

RESULT 10
US-09-559-023-2
; Sequence 2, Application US/09559023
; Patent No. 6551796
; GENERAL INFORMATION:
; APPLICANT: Abramson, Ruth
; APPLICANT: Leal-Pinto, Edgar
; APPLICANT: Lipkowitz, Michael
; TITLE OF INVENTION: NUCLEIC ACID ENCODING URATE TRANSPORTER
; FILE REFERENCE: 070165.0574
; CURRENT APPLICATION NUMBER: US/09/559,023
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/221,898
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/099,752
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/070,215
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Rat
; US-09-559-023-2

Query Match 7.1%; Score 22; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 46 AVNFOTGSGNDIAHFHPRFE 67
|||||
DB 45 AVNFOTGSGNDIAHFHPRFE 66

RESULT 11
US-08-788-584-5
; Sequence 5, Application US/08788584
; Patent No. 5837493
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Pettithory, Joanne R.
; TITLE OF INVENTION: NOVEL HUMAN GALECTINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,584
; FILING DATE: Filed Herewith
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PR-0192 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 727176
US-08-788-584-5

Query Match 6.4%; Score 20; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 7e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 IAFHLNPRFDENAVVRNTQI 239
|||||
DB 54 IAFHLNPRFDENAVVRNTQI 73

RESULT 12
US-08-946-914-12
; Sequence 12, Application US/08946914
; Patent No. 6027916
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV

; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,914
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,093
; FILING DATE: 09-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0560001/EKS/SCW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-946-914-12

Query Match 6.4%; Score 20; DB 3; Length 145;
Best Local Similarity 100.0%; Pred. No. 7e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 IAFHLNPRFDENAVVRNTQI 239
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DB 54 IAFHLNPRFDENAVVRNTQI 73

RESULT 13
US-09-656-450-12
; Sequence 12, Application US/09656450
; Patent No. 6468768
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Galectin 9 and 10SV Polynucleotides
; FILE REFERENCE: 1488.0560003
; CURRENT APPLICATION NUMBER: US/09/656,450
; CURRENT FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/263,689
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: US 08/946,914
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: US 60/028,093
; PRIOR FILING DATE: 1996-10-09
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Rat
US-09-656-450-12

Query Match 6.4%; Score 20; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 7e-12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 54 IAFHLNPRFDENAVVRNTQI 73

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US-09-557-170A-3
; Sequence 3, Application US/09557170A
; Patent No. 6605699
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Galectin 11
; FILE REFERENCE: PF354P2
; CURRENT APPLICATION NUMBER: US/09/557,170A
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 09/109,864
; PRIOR FILING DATE: 1998-06-06
; PRIOR APPLICATION NUMBER: 09/010,146
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: 60/034,205
; PRIOR FILING DATE: 1997-01-21
; PRIOR APPLICATION NUMBER: 60/034,204
; PRIOR FILING DATE: 1997-01-21
; PRIOR APPLICATION NUMBER: 60/169,932
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/130,390
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-170A-3

Query Match 6.4%; Score 20; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 7e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 54 IAFHLNPRFDENAVVRNTQI 73

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; Sequence 14, Application US/08946914
; Patent No. 6027916
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,914
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/028,093
; FILING DATE: 09-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0560001/EKS/SGW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 262 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-946-914-14

Query Match 3.9%; Score 12; DB 3; Length 262;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 GNDIAFHFNPRF 66
Db 164 GNDIAFHFNPRF 175

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Job time : 44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 07:50:39 ; Search time 1430 Seconds

(without alignments)
84.020 Million cell updates/sec

Title: US-09-263-689-4

Perfect score: 311

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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0

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- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB_PUB.pdb*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pdb*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	311	100.0	311	9	US-09-263-689-4
2	311	100.0	311	14	US-10-235-674-4
3	306	98.4	311	15	US-10-415-586-3
4	163	52.4	323	9	US-09-728-479-2
5	163	52.4	323	14	US-10-024-298A-141
6	163	52.4	323	14	US-10-042-211A-141
7	163	52.4	323	15	US-10-415-586-2
8	163	52.4	323	15	US-10-617-217A-141
9	163	52.4	323	16	US-10-024-298A-141
10	163	52.4	355	14	US-10-376-133-18
11	163	52.4	355	15	US-10-415-586-1

12	163	52.4	355	15	US-10-633-035-2
13	163	52.4	355	15	US-10-633-035-6
14	163	52.4	355	16	US-10-856-888-18
15	163	52.4	378	9	US-09-738-973-439
16	163	52.4	378	9	US-09-854-133-439
17	163	52.4	378	14	US-10-144-649A-439
18	148	47.6	168	9	US-09-922-217-199
19	148	47.6	168	9	US-09-833-283-199
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26	69	22.2	145	9	US-09-894-526-1
27	69	22.2	149	9	US-09-894-526-3
28	68	21.9	353	15	US-10-633-035-8
29	41	13.2	355	15	US-10-138-588-76
30	38	12.2	97	9	US-09-925-301-1437
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36	20	6.4	145	15	US-10-455-366-3
37	17	5.5	17	15	US-10-415-586-6
38	17	5.5	29	15	US-10-415-586-5
39	17	5.5	61	15	US-10-415-586-4
40	13	4.2	322	9	US-09-728-479-11
41	12	3.9	245	15	US-10-133-234A-6
42	12	3.9	262	9	US-09-263-689-14
43	12	3.9	262	14	US-10-235-674-14
44	12	3.9	262	15	US-10-398-519-13
45	10	3.2	39	9	US-09-975-143-12

ALIGNMENTS

RESULT 1

US-09-263-689-4
; Sequence 4, Application US/09263689
; Patent No. US20020150970A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,689
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/946,914
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0560001/EKS/SGW
; TELECOMMUNICATION INFORMATION:

Sequence 2, Appli
Sequence 6, Appli
Sequence 18, Appli
Sequence 439, App
Sequence 439, App
Sequence 439, App
Sequence 199, App
Sequence 199, App
Sequence 199, App
Sequence 143466,
Sequence 12, Appli
Sequence 7, Appli
Sequence 19, Appli
Sequence 19, Appli
Sequence 78, Appli
Sequence 1, Appli
Sequence 3, Appli
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Sequence 76, Appli
Sequence 1437, Ap
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Sequence 12, Appli
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Sequence 14, Appli
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Sequence 13, Appli
Sequence 12, Appli

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;
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 311 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-263-689-4

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Best Local Similarity 100.0%; Pred. No. 1.1e-283;
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DB 61 HFNPRFEDGGYVVCNTRQSGWGPBERKTHMPFQKGMPPDLCLVQSSDFKVMVNGILFV 120
QY 121 QYHRVPFHRVDTISVNGSVQLSYISFQOTVHTVQSAFGQMFSTPAIPPMYPHPAYP 180
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DB 181 MPFITTLGLYPSKSIILLSGTVLPSAQRPHINLCSGNHIAFHLNPRFDENAVRNTQID 240
QY 241 NSWGSEERSLPRKMPFVRGQSFVWILCEAHLKVAVDGQHLFEYHRLNLTINRLEV 300
DB 241 NSWGSEERSLPRKMPFVRGQSFVWILCEAHLKVAVDGQHLFEYHRLNLTINRLEV 300
QY 301 GGDILQLTHVQT 311
DB 301 GGDILQLTHVQT 311

RESULT 3
US-10-415-586-3
; Sequence 3, Application US/10415586
; Publication No. US20040053346A1
; GENERAL INFORMATION:
; APPLICANT: HIRASHIMA, Mitsuomi
; APPLICANT: YAMAUCHI, Akira
; APPLICANT: KAGESHITA, Toshiro
; APPLICANT: NAKAMURA, Takamori
; APPLICANT: NISHI, No. US20040053346A1om
; TITLE OF INVENTION: Predicting agent for a metastasis
; FILE REFERENCE: 2003-0572A/WMC/01332
; CURRENT APPLICATION NUMBER: US/10/415,586
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: PCT/JP01/09561
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: JP 2000-335077
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-586-3

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Best Local Similarity 100.0%; Pred. No. 5.4e-279;
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QY 246 EERSLPRKMPFVRGQSFVWILCEAHLKVAVDGQHLFEYHRLNLTINRLEVGGDIO 305
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Qy 306 LTHVQT 311
Db 306 LTHVQT 311

RESULT 4
US-09-728-479-2
; Sequence 2, Application US/09728479
; Patent No. US20020034726A1
; GENERAL INFORMATION:
; APPLICANT: KANEGASAKI, SHIRO
; APPLICANT: MATSUMOTO, RYOJI
; APPLICANT: HIRASHIMA, MITSUOMI
; TITLE OF INVENTION: EOSINOPHIL CHEMOTACTIC FACTOR
; FILE REFERENCE: 3914-2
; CURRENT APPLICATION NUMBER: US/09/728,479
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: PCT/JP99/02952
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: JP 10/170698
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-728-479-2

Query Match 52.4%; Score 163; DB 9; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.4e-144;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 269 EAHCLKVAVDQGHLEFYHRLNRLPTINRLEVGDDIQLTHVQT 311
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RESULT 5
US-10-024-298A-141
; Sequence 141, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: Goichi HONDA
; APPLICANT: Shuji MURAMATSU
; APPLICANT: Yukiko NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0089912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
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Qy 306 LTHVQT 311
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; Sequence 141, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NFkB Activating Gene
; FILE REFERENCE: 1254-0192P
; CURRENT APPLICATION NUMBER: US/10/042,211A
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
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US-10-042-211A-141

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Best Local Similarity 100.0%; Pred. No. 1.4e-144;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; SEQ ID NO 141
; LENGTH: 323
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; ORGANISM: Homo sapiens
US-10-024-298A-141

Query Match 52.4%; Score 163; DB 14; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.4e-144;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TOTVIHTVQSAPGQMFSTPAIPPMYPHPAYMPFITTILGGLYPSKILLSGTGLPSAQ 208
Db 161 TOTVIHTVQSAPGQMFSTPAIPPMYPHPAYMPFITTILGGLYPSKILLSGTGLPSAQ 220

Qy 209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWSEERSLPRKMPFVRQGSFVWILC 268
Db 221 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWSEERSLPRKMPFVRQGSFVWILC 280

Qy 269 EAHCLKVAVDQGHLEFYHRLNRLPTINRLEVGDDIQLTHVQT 311
Db 281 EAHCLKVAVDQGHLEFYHRLNRLPTINRLEVGDDIQLTHVQT 323

RESULT 6
US-10-042-211A-141
; Sequence 141, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NFkB Activating Gene
; FILE REFERENCE: 1254-0192P
; CURRENT APPLICATION NUMBER: US/10/042,211A
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 141
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-211A-141

Query Match 52.4%; Score 163; DB 14; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.4e-144;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TOTVIHTVQSAPGQMFSTPAIPPMYPHPAYMPFITTILGGLYPSKILLSGTGLPSAQ 208
Db 161 TOTVIHTVQSAPGQMFSTPAIPPMYPHPAYMPFITTILGGLYPSKILLSGTGLPSAQ 220

Qy 209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWSEERSLPRKMPFVRQGSFVWILC 268
Db 221 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWSEERSLPRKMPFVRQGSFVWILC 280

Qy 269 EAHCLKVAVDQGHLEFYHRLNRLPTINRLEVGDDIQLTHVQT 311
Db 281 EAHCLKVAVDQGHLEFYHRLNRLPTINRLEVGDDIQLTHVQT 323

RESULT 7
US-10-415-586-2
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; Sequence 2, Application US/10415586
; Publication No. US20040053346A1
; GENERAL INFORMATION:
; APPLICANT: HIRASHIMA, Mitsuomi
; APPLICANT: YAMAUCHI, Akira
; APPLICANT: KAGESHITA, Toshiro
; APPLICANT: NAKAMURA, Takanori
; APPLICANT: NISHI, No. US20040053346A1om
; TITLE OF INVENTION: Predicting agent for a metastasis
; FILE REFERENCE: 2003-0572A/WMC/01332
; CURRENT APPLICATION NUMBER: US/10/415,586
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: PCT/JP01/09561
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: JP 2000-335077
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-415-586-2

Query Match      52.4%; Score 163; DB 15; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.4e-144;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TQTVIHTVQSAGQMFSTPAIPPMYPHPAYPMPFTITILGGLYPSKILLSGTVLPSAQ 208
Db 161 TQTVIHTVQSAGQMFSTPAIPPMYPHPAYPMPFTITILGGLYPSKILLSGTVLPSAQ 220
Qy 209 RFHINLCSGNHIAFLNPRFDENAVRNTQIDNSWGSEERSLPRKMPFVRGQSFVWILC 268
Db 221 RFHINLCSGNHIAFLNPRFDENAVRNTQIDNSWGSEERSLPRKMPFVRGQSFVWILC 280
Qy 269 EAHCLKVAVDQGLFEYHRLNLPINRLEVGDDIQLTHVQT 311
Db 281 EAHCLKVAVDQGLFEYHRLNLPINRLEVGDDIQLTHVQT 323

RESULT 9
US-10-024-298A-141
; Sequence 141, Application US/10024298A
; Publication No. US20040214167A9
; GENERAL INFORMATION:
; APPLICANT: ASAHU KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: Goichi HONDA
; APPLICANT: Shuji MURAMATSU
; APPLICANT: Yukiko NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 141
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-024-298A-141

Query Match      52.4%; Score 163; DB 16; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.4e-144;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TQTVIHTVQSAGQMFSTPAIPPMYPHPAYPMPFTITILGGLYPSKILLSGTVLPSAQ 208
Db 161 TQTVIHTVQSAGQMFSTPAIPPMYPHPAYPMPFTITILGGLYPSKILLSGTVLPSAQ 220
Qy 209 RFHINLCSGNHIAFLNPRFDENAVRNTQIDNSWGSEERSLPRKMPFVRGQSFVWILC 268
Db 221 RFHINLCSGNHIAFLNPRFDENAVRNTQIDNSWGSEERSLPRKMPFVRGQSFVWILC 280
Qy 269 EAHCLKVAVDQGLFEYHRLNLPINRLEVGDDIQLTHVQT 311
Db 281 EAHCLKVAVDQGLFEYHRLNLPINRLEVGDDIQLTHVQT 323

RESULT 10
US-10-376-133-18
; Sequence 18, Application US/10376133
; Publication No. US20030165965A1
; GENERAL INFORMATION:
; APPLICANT: EXSELIXIS, INC.
; TITLE OF INVENTION: LGALS AS MODIFIERS OF THE CHK PATHWAY AND METHODS OF USE
```

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; FILE REFERENCE: EX03-014C
; CURRENT APPLICATION NUMBER: US/10/376,133
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,757
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-376-133-18

Query Match      52.4%; Score 163; DB 14; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.6e-144;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TOTVHTVQSAPGQMFSTPAIPPMYPHPAYMPFITTILGGLYPSKILLSGTVLPSSAQ 208
Db 193 TOTVHTVQSAPGQMFSTPAIPPMYPHPAYMPFITTILGGLYPSKILLSGTVLPSSAQ 252

Qy 209 RFHNLCSGNHIAFLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFWSWILC 268
Db 253 RFHNLCSGNHIAFLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFWSWILC 312

Qy 269 EAHCLKVAVDQHLFEYHRLNRLPTINRLEVGDIQLTHVQT 311
Db 313 EAHCLKVAVDQHLFEYHRLNRLPTINRLEVGDIQLTHVQT 355

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RESULT 11
US-10-415-586-1
; Sequence 1, Application US/10415586
; Publication No. US20040053346A1
; GENERAL INFORMATION:
; APPLICANT: HIRASHIMA, Mitsuomi
; APPLICANT: YAMAGUCHI, Akira
; APPLICANT: KAGESHITA, Toshiro
; APPLICANT: NAKAMURA, Takanori
; APPLICANT: NISHI, No. US20040053346A1omu
; TITLE OF INVENTION: Predicting agent for a metastasis
; FILE REFERENCE: 2003-0572A/WNC/01332
; CURRENT APPLICATION NUMBER: US/10/415,586
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: PCT/JP01/09561
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: JP 2000-335077
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-586-1

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Query Match      52.4%; Score 163; DB 15; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.6e-144;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TOTVHTVQSAPGQMFSTPAIPPMYPHPAYMPFITTILGGLYPSKILLSGTVLPSSAQ 208
Db 193 TOTVHTVQSAPGQMFSTPAIPPMYPHPAYMPFITTILGGLYPSKILLSGTVLPSSAQ 252

Qy 209 RFHNLCSGNHIAFLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFWSWILC 268
Db 253 RFHNLCSGNHIAFLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFWSWILC 312

Qy 269 EAHCLKVAVDQHLFEYHRLNRLPTINRLEVGDIQLTHVQT 311
Db 313 EAHCLKVAVDQHLFEYHRLNRLPTINRLEVGDIQLTHVQT 355

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RESULT 12
US-10-633-035-2
; Sequence 2, Application US/10633035
; Publication No. US20040068104A1
; GENERAL INFORMATION:
; APPLICANT: Seisi Kato
; APPLICANT: Yamaguchi Kimura
; APPLICANT: Shingo Sekine
; APPLICANT: Kouju Kamata
; TITLE OF INVENTION: HUMAN GALECTIC-9-LIKE PROTEINS AND cDNA ENCODING THESE
; FILE REFERENCE: GIN-6707CPUS
; CURRENT APPLICATION NUMBER: US/10/633,035
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US/09/485,951
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 9-226468
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: PCT/JP98/03670
; PRIOR FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-633-035-2

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Query Match      52.4%; Score 163; DB 15; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.6e-144;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TOTVHTVQSAPGQMFSTPAIPPMYPHPAYMPFITTILGGLYPSKILLSGTVLPSSAQ 208
Db 193 TOTVHTVQSAPGQMFSTPAIPPMYPHPAYMPFITTILGGLYPSKILLSGTVLPSSAQ 252

Qy 209 RFHNLCSGNHIAFLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFWSWILC 268
Db 253 RFHNLCSGNHIAFLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFWSWILC 312

Qy 269 EAHCLKVAVDQHLFEYHRLNRLPTINRLEVGDIQLTHVQT 311
Db 313 EAHCLKVAVDQHLFEYHRLNRLPTINRLEVGDIQLTHVQT 355

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RESULT 13
US-10-633-035-6
; Sequence 6, Application US/10633035
; Publication No. US20040068104A1
; GENERAL INFORMATION:
; APPLICANT: Seisi Kato
; APPLICANT: Yamaguchi Kimura
; APPLICANT: Shingo Sekine
; APPLICANT: Kouju Kamata
; TITLE OF INVENTION: HUMAN GALECTIC-9-LIKE PROTEINS AND cDNA ENCODING THESE
; FILE REFERENCE: GIN-6707CPUS
; CURRENT APPLICATION NUMBER: US/10/633,035
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US/09/485,951
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 9-226468
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: PCT/JP98/03670
; PRIOR FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-633-035-6

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Query Match
Best Local Similarity 52.4%; Score 163; DB 15; Length 355;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 TOTVIHTVQSAPGQMESTPAIPPMWYPHPAYPMPFFITTLGGLYPSKSIILSGTVLP
DB 193 TOTVIHTVQSAPGQMESTPAIPPMWYPHPAYPMPFFITTLGGLYPSKSIILSGTVLP
QY 209 RFHNLCSGNHIAFHLNPRDENAVVANTQIDNSWGSEERSLPRKMPPFVRGQSFVS
DB 253 RFHNLCSGNHIAFHLNPRDENAVVANTQIDNSWGSEERSLPRKMPPFVRGQSFVS
QY 269 EAHCLKVADGQHLFEYYHRLNPLTNIRLEVGGDIQLTHVQT 311
DB 313 EAHCLKVADGQHLFEYYHRLNPLTNIRLEVGGDIQLTHVQT 355

RESULT 14
US-10-856-888-18
Sequence 18, Application US/10856888
Publication No. US20040235037A1
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Polymorphic Markers of Prostate Carcinoma Tumor Antigen-1 (PCTA-1)
FILE REFERENCE: GEN-F11XCI
CURRENT APPLICATION NUMBER: US/10/856,888
CURRENT FILING DATE: 2004-05-27
PRIOR APPLICATION NUMBER: US/09/326,402
PRIOR FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 60/088,187
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/102,324
PRIOR FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 355
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(355)
OTHER INFORMATION: amino acid sequence of gal9-1
US-10-856-888-18

Query Match
Best Local Similarity 52.4%; Score 163; DB 16; Length 355;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 TOTVIHTVQSAPGQMESTPAIPPMWYPHPAYPMPFFITTLGGLYPSKSIILSGTVLP
DB 193 TOTVIHTVQSAPGQMESTPAIPPMWYPHPAYPMPFFITTLGGLYPSKSIILSGTVLP
QY 209 RFHNLCSGNHIAFHLNPRDENAVVANTQIDNSWGSEERSLPRKMPPFVRGQSFVS
DB 253 RFHNLCSGNHIAFHLNPRDENAVVANTQIDNSWGSEERSLPRKMPPFVRGQSFVS
QY 269 EAHCLKVADGQHLFEYYHRLNPLTNIRLEVGGDIQLTHVQT 311
DB 313 EAHCLKVADGQHLFEYYHRLNPLTNIRLEVGGDIQLTHVQT 355

RESULT 15
US-09-738-973-439
Sequence 439, Application US/09738973
Patent No. US20020110563A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Henderson, Robert A.
APPLICANT: Lodes, Michael J.
APPLICANT: Fling, Steven P.

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OM protein - protein search, using sw model

Run on: July 13, 2005, 07:46:47 ; Search time 174 Seconds
(without alignments)
915.268 Million cell updates/sec

Title: US-09-263-689-4
Perfect score: 311
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Gapop 60.0 , Gapext 60.0
Searched: 1612378 seqs, 512079187 residues

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Minimum DB seq length: 0
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1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	311	100.0	311	2 Q8WYQ7	Q8WYQ7 homo sapien
2	163	52.4	355	1 LEG3 HUMAN	O00182 homo sapien
3	41	13.2	356	2 Q6DKI2	Q6DKI2 homo sapien
4	22	7.1	322	2 Q6P7Q6	Q6P7Q6 rattus norv
5	22	7.1	354	1 LEG3 RAT	P97840 rattus norv
6	20	6.4	144	1 LEG3 RAT	P47967 rattus norv
7	17	5.5	323	2 Q6QZP2	Q6QZP2 canis famil
8	16	5.1	317	2 Q9XSM8	Q9XSM8 sus scrofa
9	16	5.1	349	2 Q9XSM9	Q9XSM9 sus scrofa
10	13	4.2	322	2 Q9L83	O95183 mus musculus
11	13	4.2	353	1 LEG3 MOUSE	O08573 mus musculus
12	12	3.9	244	1 LEG3 CRILLO	P47953 cricetus
13	12	3.9	261	1 LEG3 RAT	P08699 rattus norv
14	11	3.5	332	2 Q8UW97	Q8UW97 xenopus lae
15	11	3.5	353	2 Q6PGR5	Q6PGR5 xenopus lae
16	10	3.2	262	2 Q90713	Q90713 gallus gall
17	10	3.2	296	2 Q9NZ03	Q9NZ03 homo sapien
18	10	3.2	308	2 Q7ZTB8	Q7ZTB8 xenopus lae
19	10	3.2	324	1 LEG4 RAT	P38552 rattus norv
20	10	3.2	328	2 Q86G9	Q86G99 rhipicephal
21	10	3.2	328	2 Q9TUB8	Q9TUB8 oryctolagus
22	10	3.2	332	2 Q8QD9	Q8QD9 gallus gall
23	10	3.2	336	1 LEGC HUMAN	Q9EDT0 homo sapien
24	9	2.9	162	2 Q9WN59	Q9WN59 ovis aries
25	9	2.9	265	2 Q941Y9	Q941Y9 oryza sativ
26	9	2.9	503	2 Q9VPI6	Q9VPI6 dirosophila
27	8	2.6	48	2 Q9QW2	Q9QW2 rattus sp.
28	8	2.6	119	2 Q9QW3	Q85FV3 cyanidiosch
29	8	2.6	121	2 Q86TY5	Q86TY5 homo sapien
30	8	2.6	122	2 Q8KAI2	Q8KAI2 chlorobium
31	8	2.6	139	2 Q61357	Q61357 mus musculus

32	8	2.6	139	2 Q6DGI1	Q6DGI1 brachydanio
33	8	2.6	180	2 Q7T120	Q7T120 brachydanio
34	8	2.6	241	1 LEG3 RABIT	P47845 oryctolagus
35	8	2.6	249	1 LEG3 HUMAN	P17931 homo sapien
36	8	2.6	250	2 Q6FGL0	Q6FGL0 homo sapien
37	8	2.6	250	2 Q6IBA7	Q6IBA7 homo sapien
38	8	2.6	250	2 Q6NVH9	Q6NVH9 homo sapien
39	8	2.6	263	1 LEG3 MOUSE	P16110 mus musculus
40	8	2.6	264	2 Q8C253	Q8C253 mus musculus
41	8	2.6	295	1 LEG3 CANFA	P38486 canis famil
42	8	2.6	300	2 Q96Q57	Q96Q57 homo sapien
43	8	2.6	301	1 LEG6 MOUSE	O54891 mus musculus
44	8	2.6	310	2 Q6PBV2	Q6PBV2 brachydanio
45	8	2.6	310	2 Q7T118	Q7T118 brachydanio

ALIGNMENTS

RESULT 1
Q8WYQ7
ID Q8WYQ7 PRELIMINARY; PRT; 311 AA.
AC Q8WYQ7;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Galectin-9.
GN Name=LGALS9;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Akiyama S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the galectin (galaptin/S-lectin) family.
DR EMBL; AB040130; BAB83623.1; -.
DR EMBL; AB040129; BAB83623.1; JOINED.
DR HSSP; P17931; 1A3K.
DR GO; GO:0005529; F:sugar binding; IEA.
DR Pfam; PF00337; Gal-bind_lectin; 2.
DR SMART; SM00276; GLECT; 2.
DR PROSITE; PS00309; GALAPTIN; 2.
KW Galectin; Lectin.
SQ SEQUENCE 311 AA; 34690 MW; 3D00232FE39D776C CRC64;

Query Match	100.0%;	Score 311;	DB 2;	Length 311;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 311;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAFSGSQAPYLSAPVPSFGT	100.0%;	Score 311;
Db	1	MAFSGSQAPYLSAPVPSFGT	100.0%;	Score 311;
Qy	61	HNFRPFEDGGVVCNTRQNGSWGPEERKTHMPFKGMFPDLCFLVQSSDFKVMVNGILFV	120	
Db	61	HNFRPFEDGGVVCNTRQNGSWGPEERKTHMPFKGMFPDLCFLVQSSDFKVMVNGILFV	120	
Qy	121	QYFHRVFPFHRVDTTISVNGSVQLSYISFQTQVTHVTSAPQCMFSTPAIPMMVPHPAYP	180	
Db	121	QYFHRVFPFHRVDTTISVNGSVQLSYISFQTQVTHVTSAPQCMFSTPAIPMMVPHPAYP	180	
Qy	181	MPFTTITLGGLYPSKILLSGTVLPSAQRHINLCSGNHIAFHLNPRFENAVRNTQID	240	
Db	181	MPFTTITLGGLYPSKILLSGTVLPSAQRHINLCSGNHIAFHLNPRFENAVRNTQID	240	
Qy	241	NSWSEERSLPKMPFVRGQSFVWILCEAHLKVAVDGQHLFEYHRLNLPINRLEV	300	
Db	241	NSWSEERSLPKMPFVRGQSFVWILCEAHLKVAVDGQHLFEYHRLNLPINRLEV	300	
Qy	301	GGDIQLTHVQT	311	
Db	301	GGDIQLTHVQT	311	

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Db 301 GGDQLTHVQT 311
LEG9 HUMAN
RESULT 2
ID LEG9 HUMAN STANDARD; PRT; 355 AA.
AC O00182; O14532; O75028; Q9NQ58;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Galectin-9 (HOM-HD-21) (Ecalectin).
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC TISSUE=Spleen;
RX MEDLINE=97197815; PubMed=9045665; DOI=10.1074/jbc.272.10.6416;
RA Tuercii O., Schmitt H., Fadle N., Pfreundschuh M., Sahin U.;
RT "Molecular definition of a novel human galectin which is immunogenic
in patients with Hodgkin's disease.";
RL J. Biol. Chem. 272:6416-6422 (1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC TISSUE=Gastric carcinoma;
RA Kato S.;
RN Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=98307937; PubMed=9642261; DOI=10.1074/jbc.273.27.16976;
RA Matsumoto R., Matsumoto H., Seki M., Hata M., Asano Y., Kanegasaki S.,
RA Stevens R.L., Hirashima M.;
RT "Human ecalectin, a variant of human galectin-9, is a novel eosinophil
chemoattractant produced by T lymphocytes.";
RL J. Biol. Chem. 273:16976-16984 (1998).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RA Akiyama S.;
RT "Homo sapiens galectin-9 (LGALS9) / ecalectin gene, exon 2 through
11.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RA Graessler J., Spitzenberger F., Schroeder H.E.;
RT "Genomic organization of the human galectin-9 gene.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Binds galactosides. May play a role in thymocyte-
epithelial interactions relevant to the biology of the thymus. The
short isoform acts as an eosinophil chemoattractant.
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=Long;
IsoId=O00182-1; Sequence=Displayed;
Name=Short;
IsoId=O00182-2; Sequence=VSP 003096;
CC -1- TISSUE SPECIFICITY: Peripheral blood leukocytes and lymphatic
tissues. Overexpressed in Hodgkin's disease tissue.
CC -1- DOMAIN: Contains two homologous but distinct carbohydrate-binding
domains.
CC -1- SIMILARITY: Belongs to the galectin (galaptin/S-lectin) family.
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EMBL; Z49107; CAA88922.1; -.

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DR EMBL; AB006782; BAA22166.1; -.
DR EMBL; AB005894; BAA31542.1; -.
DR EMBL; AB040130; BAB83625.1; -.
DR EMBL; AB040129; BAB83625.1; JOINED.
DR EMBL; AB040130; BAB83624.1; -.
DR EMBL; AB040129; BAB83624.1; JOINED.
DR EMBL; AJ288083; CAB93851.1; -.
DR EMBL; AJ288084; CAB93851.1; JOINED.
DR EMBL; AJ288085; CAB93851.1; JOINED.
DR EMBL; AJ288086; CAB93851.1; JOINED.
DR EMBL; AJ288087; CAB93851.1; JOINED.
DR EMBL; AJ288088; CAB93851.1; JOINED.
DR EMBL; AJ288089; CAB93851.1; JOINED.
DR EMBL; AJ288090; CAB93851.1; JOINED.
DR HSSP; P17931; 1A3K.
DR Gnew; HGNC:6570; LGALS9.
DR MIM; 601879; -.
DR GO; GO:0005534; F:galactose binding; TAS.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR001079; Galectin.
DR Pfam; PF00337; Gal-bind lectin; 2.
DR PROSITE; PS00309; GALAPTIN; 2.
KW Alternative splicing; Galectin; Lectin; Repeat.
FT DOMAIN 1 148 Galaptin 1.
FT DOMAIN 149 206 Linker.
FT DOMAIN 207 355 Galaptin 2.
FT SITE 82 88 Beta-galactoside binding 1 (By
similarity).
FT SITE 287 293 Beta-galactoside binding 2 (By
similarity).
FT VARSPLIC 149 180 Missing (in isoform Short).
FT CONFLICT 5 5 G -> S (in Ref. 3).
FT CONFLICT 48 48 N -> D (in Ref. 5).
FT CONFLICT 79 81 NGS -> KGR (in Ref. 5).
FT CONFLICT 88 88 K -> R (in Ref. 1).
FT CONFLICT 89 89 T -> M (in Ref. 5).
FT CONFLICT 135 135 S -> F (in Ref. 1).
FT CONFLICT 270 270 P -> L (in Ref. 1).
FT CONFLICT 313 313 E -> G (in Ref. 1).
FT CONFLICT 326 326 L -> V (in Ref. 5).
FT CONFLICT 341 341 R -> K (in Ref. 5).
SQ SEQUENCE 355 AA; 39518 MW; 4748C222FCFAF536A CRC64;
Query Match 52.4%; Score 163; DB 1; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.7e-162;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 149 TOTVIHTVQSAPQGMFSTPAIPPMYPHPAYPMPPFITTLGGLYPSKSIILSGTVLP5AQ 208
Db 193 TQVIHTVQSAPQGMFSTPAIPPMYPHPAYPMPPFITTLGGLYPSKSIILSGTVLP5AQ 252
Qy 209 RFHINLCSGNHIAFHLPNPRDENAVRNTQIDNSWGSEERSLPRKMPFVRGQSF5WILC 268
Db 253 RFHINLCSGNHIAFHLPNPRDENAVRNTQIDNSWGSEERSLPRKMPFVRGQSF5WILC 312
Qy 269 EAHCLKVAVDQGHLEFYHRLNLPINRLEVGGDIQLTHVQT 311
Db 313 EAHCLKVAVDQGHLEFYHRLNLPINRLEVGGDIQLTHVQT 355
RESULT 3
O6DKI2 PRELIMINARY; PRT; 356 AA.
ID O6DKI2
AC O6DKI2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fabey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RA [2]
RA SEQUENCE FROM N.A.
RA TISSUE=Pituitary gland;
RA Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the galectin (galactin/S-lectin) family.
DR EMBL; BC03889; AAH3889.1; -;
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR001079; Galectin.
DR Pfam; PF00337; Gal-bind lectin; 2.
DR SMART; SM00276; GLECT; 2.
DR PROSITE; PS00309; GALAPTIN; 2.
KW Galectin; Hypothetical protein; Lectin.
SQ SEQUENCE 356 AA; 39633 MW; 933AD3A82B84784C CRC64;

Query Match 13.2%; Score 41; DB 2; Length 356;
Best Local Similarity 100.0%; Pred. No. 4.7e-34; Indels 0; Gaps 0;
Matches 41; Conservative 0; Mismatches 0;

Qy 241 NSWGSEERSLRKMPFVRGQSFVWILCEAHLKVAVDQGH 281
Db 286 NSWGSEERSLRKMPFVRGQSFVWILCEAHLKVAVDQGH 326

RESULT 4
Q6P7Q6 PRELIMINARY; PRT; 322 AA.
ID Q6P7Q6
AC Q6P7Q6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Lectin, galactose binding, soluble 9.
GN Name=Lgale9;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Pituitary gland;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fabey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RA [2]
RA SEQUENCE FROM N.A.
RA TISSUE=Pancreas;
RA Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the galectin (galactin/S-lectin) family.
DR EMBL; BC03889; AAH3889.1; -;
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR001079; Galectin.
DR Pfam; PF00337; Gal-bind lectin; 2.
DR SMART; SM00276; GLECT; 2.
DR PROSITE; PS00309; GALAPTIN; 2.
KW Galectin; Hypothetical protein; Lectin.
SQ SEQUENCE 356 AA; 39633 MW; 933AD3A82B84784C CRC64;

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fabey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RA [2]
RA SEQUENCE FROM N.A.
RA TISSUE=Pituitary gland;
RA Strausberg R.;
RA Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the galectin (galactin/S-lectin) family.
DR EMBL; BC061566; AAH61566.1; -;
DR HSBP; P17931; 1A3K.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR001079; Galectin.
DR Pfam; PF00337; Gal-bind lectin; 2.
DR SMART; SM00276; GLECT; 2.
DR PROSITE; PS00309; GALAPTIN; 2.
KW Galectin; Lectin.
SQ SEQUENCE 322 AA; 36341 MW; CDD414A6FD1BA9DD CRC64;

Query Match 7.1%; Score 22; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.3e-14; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;

Qy 46 AVNFQTGSGNDIAFHFNPRFE 67
Db 45 AVNFQTGSGNDIAFHFNPRFE 66

RESULT 5
LEG9 RAT
ID LEG9 RAT STANDARD; PRT; 354 AA.
AC P97840; O08588; O35866;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Galectin-9 (36 kDa beta-galactoside binding lectin) (Urate
DE transporter/channel) (UAT).
GN Name=Lgale9;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RX STRAIN=Sprague-Dawley; TISSUE=Kidney, and Small intestine;
RX MEDLINE=97190351; PubMed=9038233; DOI=10.1074/jbc.272.9.6078;
RA Wada J., Kanwar Y.S.;
RA "Identification and characterization of galectin-9, a novel beta-
RA galactoside-binding mammalian lectin.";
RA J. Biol. Chem. 272:617-625(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=97150769; PubMed=895305; DOI=10.1074/jbc.272.1.617;
RA Leal-Pinto E., Tao W., Rappaport J., Richardson M., Knorr B.A.,
RA Abramson R.G.;
RA "Molecular cloning and functional reconstitution of a urate
RA transporter/channel.";
RA J. Biol. Chem. 272:617-625(1997).
CC -!- FUNCTION: Binds galactosides. May play a role in thymocyte-
CC epithelial interactions relevant to the biology of the thymus (By
CC similarity). May provide the molecular basis for urate flux across

cell membranes, allowing urate that is formed during purine metabolism to efflux from cells and serving as an electrogenic transporter that plays an important role in renal and gastrointestinal urate excretion. Highly selective to the anion urate.

CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic. May also be secreted by a non-classical secretory pathway (By similarity).

CC CC -1- ALTERNATIVE PRODUCTS:

CC CC Event=Alternative splicing; Named isoforms=2;

CC CC Comment=Additional isoforms seem to exist;

CC CC Name=Long;

CC CC IsoId=P97840-1; Sequence=Displayed;

CC CC Name=Short;

CC CC IsoId=P97840-2; Sequence=VSP_003098;

CC CC -1- TISSUE SPECIFICITY: The long form is expressed exclusively in the small intestine.

CC CC -1- DOMAIN: Contains two homologous but distinct carbohydrate-binding domains.

CC CC -1- SIMILARITY: Belongs to the galectin (galaptin/s-lectin) family.

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CC CC -----

DR EMBL; U59462; AAB51192.1; -;

DR EMBL; U72741; AAB68592.1; -;

DR EMBL; U67958; AAB48591.1; -;

DR HSSP; P17931; IA3K.

DR RGD; 3005; Lgal9.

DR InterPro; IPR008985; ConA_like_lect_gl.

DR InterPro; IPR001079; Galectin.

DR Pfam; PF00337; Gal-bind_lectin; 2.

DR PROSITE; PS00309; GALAPTIN; 2.

DR Alternative splicing; Galectin; Ion transport; Lectin; Repeat.

FT DOMAIN 1 147 Galaptin 1.

FT DOMAIN 148 205 Linker.

FT DOMAIN 206 354 Beta-galactoside binding 1 (By similarity).

FT SITE 81 87 Beta-galactoside binding 2 (By similarity).

FT SITE 286 292 Missing (in isoform Short).

FT VARSPLIC 148 179 /FTid=VSP_003098.

FT SEQUENCE 354 AA; 39946 MW; 6574F960B2EAF37C CRC64;

Query Match 7.1%; Score 22; DB 1; Length 354;

Best Local Similarity 100.0%; Pred. No. 4.7e-14;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 AVNFQTGFGNDIAFHNPRFE 67

Db 45 AVNFQTGFGNDIAFHNPRFE 66

RESULT 6

LEG5 RAT

ID LEG5 RAT STANDARD; PRT; 144 AA.

AC P47967;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Galectin-5 (RL-18).

GN Name=Lgals5;

OS Rattus norvegicus (Rat).

OC Eukaryota; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

TISSUE=Reticulocytes;

MDLINE=95197487; PubMed=7890611; DOI=10.1074/jbc.270.10.5032;

RA Gitt M.A., Wiser M.F., Jeffler H., Herrmann J., Xia Y.-R., Massa S.M., Cooper D.N.W., Lusia A.J., Barondes S.H.;

RT "Sequence and mapping of galectin-5, a beta-galactoside-binding lectin, found in rat erythrocytes.";

RL J. Biol. Chem. 270:5032-5038(1995).

CC -1- FUNCTION: May function in erythrocyte differentiation.

CC -1- SUBUNIT: Monomer.

CC -1- TISSUE SPECIFICITY: Erythrocytes.

CC -1- SIMILARITY: Belongs to the galectin (galaptin/s-lectin) family.

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CC CC -----

DR EMBL; L36862; AAC42050.1; -;

DR EMBL; L21711; AAA65445.1; -;

DR PIR; A55932; A55932.

DR HSSP; P47929; IBKZ.

DR RGD; 3004; Lgals5.

DR InterPro; IPR008985; ConA_like_lect_gl.

DR InterPro; IPR001079; Galectin.

DR Pfam; PF00337; Gal-bind_lectin; 1.

DR SMART; SM00276; GLECT; 1.

DR PROSITE; PS00309; GALAPTIN; 1.

KW Acetylation; Direct protein sequencing; Galectin; Lectin.

FT INIT MET 0

FT SITE 76 82 Beta-galactoside binding (Potential).

FT MOD_RES 1 1 N-acetylserine.

FT CONFLICT 127 135 Missing (in Ref. 1; AAA65445).

FT SEQUENCE 144 AA; 16065 MW; BC95283D760DA515 CRC64;

Query Match 6.4%; Score 20; DB 1; Length 144;

Best Local Similarity 100.0%; Pred. No. 2.6e-12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 220 IAFHLNPRFDENAVVRNTQI 239

Db 53 IAFHLNPRFDENAVVRNTQI 72

RESULT 7

Q6QZP2

ID Q6QZP2 PRELIMINARY; PRT; 323 AA.

AC Q6QZP2;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Galectin 9.

GN Name=UAT;

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RA Bannasch D.L., Ryun J.R., Bannasch M.J., Schaible R.H., Breen M., Ling G.;

RT "Exclusion of galectin 9 as a candidate gene for hyperuricosuria in the Dalmatian dog.";

RL Anim. Genet. 35:326-328(2004).

CC -1- SIMILARITY: Belongs to the galectin (galaptin/s-lectin) family.

DR EMBL; AY521549; AAS80311.1; -;

DR HSSP; P17931; IA3K.

DR GO; GO:0005529; F:sugar binding; IEA.

DR InterPro; IPR008985; ConA_like_lect_gl.

DR InterPro; IPR001079; Galectin.

DR Pfam; PF00337; Gal-bind_lectin; 2.


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DR SMART; SM00276; GLECT; 2.
DR PROSITE; PS00309; GALAPTIN; 2.
KW Galactin; Lectin.
SQ SEQUENCE 323 AA; 36026 MW; 2C4FA3644A0EB64F CRC64;

Query Match      5.1%; Score 17; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 7.9e-09; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;

QY 241 NSWGSEERSLPKMPFV 257
Db 253 NSWGSEERSLPKMPFV 269
|||||
|||||

RESULT 8
Q9XSM8 PRELIMINARY; PRT; 317 AA.
AC Q9XSM8;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Urate transporter/channel protein (UATp).
GN Name=uatp;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=21554766; PubMed=11698107; DOI=10.1016/S0300-9084(01)01335-9;
RA Spitzberger F., Graessler J., Schroeder H.E.;
RT "Molecular and functional characterization of galactin 9 mRNA isoforms in porcine and human cells and tissues.";
RL Biochimie 83:851-862(2001).
CC -!- SIMILARITY: Belongs to the galactin (galaptin/S-lectin) family.
C1 Biochimie 83:851-862(2001).
CL Biochimie 83:851-862(2001).
CC -!- SIMILARITY: Belongs to the galactin (galaptin/S-lectin) family.
DR EMBL; AJ11826; CAB4278.1; -.
DR HSSP; P11116; ISLT.
GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR001079; Galactin.
PFam; PF00337; Gal-bind lectin; 2.
SMART; SM00276; GLECT; 2.
PROSITE; PS00309; GALAPTIN; 1.
KW Galactin; Lectin.
SQ SEQUENCE 317 AA; 35342 MW; AA09562C4B7B8B80 CRC64;

Query Match      5.1%; Score 16; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 8.8e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0;

QY 274 KVAVDGQHLFEYHRL 289
Db 286 KVAVDGQHLFEYHRL 301
|||||
|||||

RESULT 9
Q9XSM9 PRELIMINARY; PRT; 349 AA.
AC Q9XSM9;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Urate transporter/channel protein, isoform (UATp,i).
GN Name=uatp.i;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=21554766; PubMed=11698107; DOI=10.1016/S0300-9084(01)01335-9;

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RA Spitzberger F., Graessler J., Schroeder H.E.;
RT "Molecular and functional characterization of galactin 9 mRNA isoforms in porcine and human cells and tissues.";
RL Biochimie 83:851-862(2001).
CC -!- SIMILARITY: Belongs to the galactin (galaptin/S-lectin) family.
C1 Biochimie 83:851-862(2001).
CL Biochimie 83:851-862(2001).
CC -!- SIMILARITY: Belongs to the galactin (galaptin/S-lectin) family.
DR EMBL; AJ11827; CAB44279.1; -.
DR HSSP; P11116; ISLT.
GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR008985; ConA_like_lect_gl.
DR InterPro; IPR001079; Galactin.
PFam; PF00337; Gal-bind lectin; 2.
SMART; SM00276; GLECT; 2.
PROSITE; PS00309; GALAPTIN; 1.
KW Galactin; Lectin.
SQ SEQUENCE 349 AA; 38899 MW; BF83D3E213E7B64C CRC64;

Query Match      5.1%; Score 16; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 9.6e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0;

QY 274 KVAVDGQHLFEYHRL 289
Db 318 KVAVDGQHLFEYHRL 333
|||||
|||||

RESULT 10
Q99L83 PRELIMINARY; PRT; 322 AA.
AC Q99L83;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Lgal9 protein.
GN Name=Lgal9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins E.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the galactin (galaptin/S-lectin) family.
DR EMBL; BC003754; AA03754.1; -.
DR HSSP; P17931; 1A3K.
DR MGD; MGI:109496; Lgal9.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008985; ConA_like_lect_gl.

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DR InterPro; IPR001079; Galectin.
DR Pfam; PF00337; Gal-bind lectin; 2.
DR SMART; SM00276; GLECT; 2.
DR PROSITE; PS00309; GALAPTIN; 2.
KW Galectin; Lectin.
SQ SEQUENCE 322 AA; 36545 MW; 032D77400737562E CRC64;

Query Match 4.2%; Score 13; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 GNDIAFHFNPRFE 67
Db 54 GNDIAFHFNPRFE 66

RESULT 11
LEG9 MOUSE
ID LEG9 MOUSE STANDARD; PRT; 353 AA.
AC O08573; O08572;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Galectin-9.
GN Name=Lgale9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=Kidney, and Small intestine;
RX MEDLINE=97190351; PubMed=5038233; DOI=10.1074/jbc.272.9.6078;
RA Wada J., Kanwar Y.S.;
RT "Developmental regulation, expression, and apoptotic potential of
galectin-9, a beta-galactoside binding lectin.";
RL J. Clin. Invest. 99:2452-2461(1997).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=97298141; PubMed=9153289;
RA Wada J., Ota K., Kumar A., Wallner E.I., Kanwar Y.S.;
RT "Developmental regulation, expression, and apoptotic potential of
galectin-9, a beta-galactoside binding lectin.";
RL J. Clin. Invest. 99:2452-2461(1997).
CC -1- FUNCTION: Binds galactosides. May play a role in thymocyte-
epithelial interactions relevant to the biology of the thymus.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic. May also be secreted by a non-
classical secretory pathway.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Names=Long;
CC IsoId=O08573-1; Sequence=Displayed;
CC Names=Short;
CC IsoId=O08573-2; Sequence=VSP_003097;
CC -1- TISSUE SPECIFICITY: Accentuated expression in liver and thymus of
embryo, detected in embryonic heart, brain, lung, liver, and
kidney. Highly expressed in adult thymus, small intestine, and
liver, and to a lesser extent in lung, kidney, spleen, cardiac,
and skeletal muscle. Barely detectable in brain and reticulocyte.
CC The long form is expressed exclusively in the small intestine.
CC -1- DEVELOPMENTAL STAGE: The expression increased with successive
stages of embryonic development.
CC -1- DOMAIN: Contains two homologous but distinct carbohydrate-binding
domains.
CC -1- SIMILARITY: Belongs to the galectin (galaptin/S-lectin) family.
CC
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CC -----
CC EMBL; U55061; AAB51190.1; -.
CC EMBL; U55060; AAB51189.1; -.
CC HSSP; P17931; IA3K.
CC MGD; MGI:109496; Igals9.
CC InterPro; IPR008985; ConA_like_lect_gl.
CC Pfam; PF00337; Gal-bind lectin; 2.
CC PROSITE; PS00309; GALAPTIN; 2.
KW Alternative splicing; Galectin; Lectin; Repeat.
FT DOMAIN 1 147 Galaptin 1.
FT DOMAIN 148 204 Linker.
FT DOMAIN 205 353 Galaptin 2.
FT SITE 81 87 Beta-galactoside binding 1 (By
similarity).
FT SITE 285 291 Beta-galactoside binding 2 (By
similarity).
FT VARSPLIC 148 178 Missing (in isoform Short).
FT FTID=VSP_003097.
SQ SEQUENCE 353 AA; 40036 MW; B54036F6E280C531 CRC64;

Query Match 4.2%; Score 13; DB 1; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 GNDIAFHFNPRFE 67
Db 54 GNDIAFHFNPRFE 66

RESULT 12
LEG3 CRILLO
ID LEG3 CRILLO STANDARD; PRT; 244 AA.
AC P47953;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Galectin-3 (Galactose-specific lectin 3) (Mac-2 antigen) (IgE-binding
protein) (35 kDa lectin) (Carbohydrate binding protein 35) (CBP 35)
DE (Laminin-binding protein) (Lectin L-29) (CBP30).
GN Name=LGALS3;
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=94299546; PubMed=8027086;
RA Mehul B., Bawumia S., Martin S.R., Hughes R.C.;
RT "Structure of baby hamster kidney carbohydrate-binding protein CBP30,
an S-type animal lectin.";
RL J. Biol. Chem. 269:18250-18258(1994).
CC -1- FUNCTION: Galactose-specific lectin which binds IgE.
CC -1- SIMILARITY: In the C-terminal section; belongs to the galectin
(galaptin/S-lectin) family.
CC
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CC
CC EMBL; X78879; CAA55479.1; -.
CC HSSP; P17931; IA3K.
CC InterPro; IPR008985; ConA_like_lect_gl.
CC Pfam; PF00337; Gal-bind lectin; 1.
CC PROSITE; PS00309; GALAPTIN; 1.

```

KW Acetylation; Galectin; IgE-binding protein; Lectin; Phosphorylation;
 KW Repeat.
 FT INIT MET 0 0 By similarity.
 FT SITE 175 181 Beta-galactoside binding (By similarity).
 FT MOD_RES 1 1 N-acetylgalactoside binding (By similarity).
 FT MOD_RES 5 5 Phosphoserine (by CK1) (By similarity).
 FT DOMAIN 34 98 7 X 9 AA tandem repeats of Y-P-G-X(3)-P-[GS]-A.
 FT REPEAT 34 42 1.
 FT REPEAT 43 51 2.
 FT REPEAT 52 60 3.
 FT REPEAT 61 69 4.
 FT REPEAT 70 77 5 (approximate).
 FT REPEAT 78 87 6 (approximate).
 FT REPEAT 88 98 7 (approximate).
 FT DOMAIN 112 244 Galactin.
 FT DISULFID 167 167 Interchain (By similarity).
 SQ SEQUENCE 244 AA; 25608 MW; 8F99B9AA0BBA7D3F CRC64;
 Query Match 3.9%; Score 12; DB 1; Length 244;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 55 GNDIAFHENPRF 66
 Db 146 GNDIAFHENPRF 157
 |||||
 RESULT 13
 LEG3_RAT
 ID_LEG3_RAT STANDARD; PRT; 261 AA.
 AC P08699;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Galectin-3 (Galactose-specific lectin 3) (Mac-2 antigen) (IgE-binding protein) (35 kDa lectin) (carbohydrate binding protein 35) (CBP 35)
 DE (Laminin-binding protein) (lectin L-29).
 GN Name=Lgale3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88016189; PubMed=2958848;
 RA Albrandt K., Orida N.K., Liu P.-T.;
 RT "An IgE-binding protein with a distinctive repetitive sequence and homology with an IgG receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6859-6863 (1987).
 RN [2]
 RP SEQUENCE OF 124-261 FROM N.A.
 RX MEDLINE=85216641; PubMed=3858867;
 RA Liu F.-T., Albrandt K., Mendel E., Kulczycki A. Jr., Orida N.K.;
 RT "Identification of an IgE-binding protein by molecular cloning.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4100-4104 (1985).
 RN [3]
 RP SEQUENCE OF 119-144.
 RX MEDLINE=90105471; PubMed=2605254;
 RA Lefler H., Masiarz F.R., Barondes S.H.;
 RT "Soluble lactose-binding vertebrate lectins: a growing family.";
 RL Biochemistry 28:9222-9229 (1989).
 RN [4]
 RP PARTIAL SEQUENCE, AND ACETYLATION.
 RX MEDLINE=94075368; PubMed=8253805;
 RA Herrmann J., Turck C.W., Achison R.E., Huflejt M.E., Poulter L., Gitt M.A., Burlingame A.L., Barondes S.H., Lefler H.;
 RT "Primary structure of the soluble lactose binding lectin L-29 from rat and dog and interaction of its non-collagenous proline-, glycine-, tyrosine-rich sequence with bacterial and tissue collagenase.";
 RL J. Biol. Chem. 268:26704-26711 (1993).
 CC -!- FUNCTION: Galactose-specific lectin which binds IgE.
 CC -!- SUBUNIT: Probably forms homo- or heterodimers. Binds LGALS3BP (By

CC similarity).
 CC -!- SIMILARITY: In the C-terminal section; belongs to the galectin (galactin/S-lectin) family.
 CC -----
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 CC -----
 DR EMBL; J02962; AAA40828.1; -;
 DR EMBL; M13697; AAA41378.1; -;
 DR PIR; A54889; A54889.
 DR HSSP; P17931; IAKK.
 DR RGD; 69356; Lgale3.
 DR InterPro; IPR008985; ConA like_lec_gl.
 DR InterPro; IPR001079; Galectin.
 DR Pfam; PF00337; Gal-bind_lectin; 1.
 DR PROSITE; PS00309; GALAPTIN; 1.
 KW Acetylation; Direct protein sequencing; Galectin; IgE-binding protein; Lectin; Phosphorylation; Repeat.
 FT INIT_MET 0 0
 FT SITE 192 198 Beta-galactoside binding (By similarity).
 FT MOD_RES 1 1 N-acetylgalactoside.
 FT MOD_RES 5 5 Phosphoserine (by CK1) (By similarity).
 FT DOMAIN 34 111 9 X 9 AA tandem repeats of Y-P-G-X(3)-P-[GS]-[AG].
 FT REPEAT 34 42 1.
 FT REPEAT 43 51 2.
 FT REPEAT 52 60 3.
 FT REPEAT 61 69 4.
 FT REPEAT 70 78 5.
 FT REPEAT 79 87 6.
 FT REPEAT 88 97 7 (approximate).
 FT REPEAT 98 104 8 (approximate).
 FT REPEAT 105 111 9 (incomplete).
 FT DOMAIN 129 261 Galaptin.
 FT DISULFID 184 184 Interchain (By similarity).
 FT CONFLICT 19 19 Q -> R (in Ref. 1).
 SQ SEQUENCE 261 AA; 27070 MW; EAPAL17F5EA5080D CRC64;
 Query Match 3.9%; Score 12; DB 1; Length 261;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 55 GNDIAFHENPRF 66
 Db 163 GNDIAFHENPRF 174
 |||||
 RESULT 14
 Q8UW97
 ID Q8UW97 PRELIMINARY; PRT; 332 AA.
 AC Q8UW97;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Galectin family xgalectin-IVa.
 GN Name=xgalectin-IVa;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Liver;
 RX MEDLINE=21968527; PubMed=11971860; DOI=10.1093/glycob/12.3.163;
 RA Shoji H., Nishi N., Hirashima M., Nakamura T.;
 RT "Purification and cDNA cloning of Xenopus liver galectins and their expression.";

```
RL Glycobiology 12:163-172(2002).
CC -!- SIMILARITY: Belongs to the galectin (galaptin/s-lectin) family.
DR EMBL; AB060972; BAB83259.1; -.
DR HSPSP; P17931.1A3K.
DR GO; GO:0005529; F:sugar binding; IEA.
DR Pfam; PF00337; Gal-bind lectin; 2.
DR SMART; SM00276; GLECT; 2.
KW Galectin; Lectin.
SQ SEQUENCE 332 AA; 36822 MW; D273F8D35484E9C2 CRC64;

Query Match 3.5%; Score 11; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 NDIAFHFNPRF 66
Db |||||
50 NDIAFHFNPRF 60

RESULT 15
O6PGR5 PRELIMINARY; PRT; 353 AA.
AC Q6PGR5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Xgalectin-iva protein (Fragment).
GN Name=xgalectin-iva;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391(2002).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Klein S., Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the galectin (galaptin/s-lectin) family.
DR EMBL; BC056859; AAH56859.1; -.

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```
DR HSPSP; P17931.1A3K.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008985; ConA_like_lect_gl.
DR InterPro; IPR01079; Galectin.
DR Pfam; PF00337; Gal-bind lectin; 2.
DR SMART; SM00276; GLECT; 2.
KW Galectin; Lectin.
FT NON TER 1
SQ SEQUENCE 353 AA; 39242 MW; 0453CD44E93DB1C6 CRC64;

Query Match 3.5%; Score 11; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 NDIAFHFNPRF 66
Db |||||
71 NDIAFHFNPRF 81

Search completed: July 13, 2005, 08:01:45
Job time : 177 secs

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CC sequence was deduced from a human adult pancreatic tumour cDNA clone (see
CC AA29786). Novel galectins 8, 9, 10 and 10 splice variant (10SV) are
CC Claimed (see AA56503-06). These can be obtained using a claimed method
CC by expression in recombinant host cells. The novel galectins are used in
CC a claimed method for treating a cell growth disorder, especially cancer,
CC autoimmune diseases, inflammatory diseases, asthma, and allergic
CC diseases, in a mammal. They are especially useful for diagnosis of
CC melanoma, renal astrocytoma, Hodgkin disease, and breast, ovarian,
CC prostate, bone, liver, lung, pancreatic and splenic cancers. The
CC invention further relates to screening methods for identifying agonists
CC and antagonists of galectin 8, 9, 20 or 10SV activity, and to diagnostic
CC methods involving estimating levels of galectin 8, 9, 10 or 10SV protein
CC or mRNA
XX
SQ Sequence 311 AA;

Query Match 100.0%; Score 311; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 4.1e-305;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFSGQAPYLSPAVPESGTTQGGLODGLQITVNGTVLSSGTRFAVNFOTGSGNDIAF 60
DB 1 MAFSGQAPYLSPAVPESGTTQGGLODGLQITVNGTVLSSGTRFAVNFOTGSGNDIAF 60
QY 61 HFNPRFEDGGYVVCNTRQNSWGPEERKTHMPFQKGMPPFDLCFLVQSSDFKVMVNGILFV 120
DB 61 HFNPRFEDGGYVVCNTRQNSWGPEERKTHMPFQKGMPPFDLCFLVQSSDFKVMVNGILFV 120
QY 121 QYFHRVDFHRVDTISVNGSVQLSYISFQTVIHTVQSAFGQMFSTPAIPPMYPHPAYP 180
DB 121 QYFHRVDFHRVDTISVNGSVQLSYISFQTVIHTVQSAFGQMFSTPAIPPMYPHPAYP 180
QY 181 MPFTITLGLYPSKILLSGTVLPFAORPHINLCGNHIAFHLNPRFDENAVVRNTQID 240
DB 181 MPFTITLGLYPSKILLSGTVLPFAORPHINLCGNHIAFHLNPRFDENAVVRNTQID 240
QY 241 NSWGSEERSLPKMPFVRGQSFVWILCEAHCLKVAVDGQHLFEYHRLNLPINRLEV 300
DB 241 NSWGSEERSLPKMPFVRGQSFVWILCEAHCLKVAVDGQHLFEYHRLNLPINRLEV 300
QY 301 GGDITLTHVQT 311
DB 301 GGDITLTHVQT 311

RESULT 2
ABB77854
ID ABB77854 standard; protein; 311 AA.

XX
AC ABB77854;
XX
DT 27-SEP-2002 (first entry)
XX
XX Amino acid sequence of a human protein.
DE
KW Cancer; galectin 9; antibody; skin cancer; melanoma; breast cancer;
KW ovarian cancer; uterus cancer; tumour; prostate cancer; bladder cancer;
KW kidney cancer; thyroid cancer; throat cancer; tongue cancer;
KW upper jaw cancer; esophageal cancer; stomach cancer; colon cancer;
KW lung cancer; liver cancer; gall-bladder cancer; pancreatic cancer;
KW leukemia; liposarcoma; glioma.
XX
OS Homo sapiens.
XX
PN WO200237114-A1.
XX
PD 10-MAY-2002.
XX
PF 31-OCT-2001; 2001WO-JP009561.
XX
PR 01-NOV-2000; 2000JP-00335077.
XX
PA (GALP-) GALPHARMA CO LTD.

XX Hirashima M, Yamauchi A, Kageshita T, Nakamura T, Nishi N;
XX WPI; 2002-519265/55.
XX
XX Metastasis mechanism-based agents (anti-galectin 9 antibody) for
PT detecting ability of cancer to metastasize in cells, uses galectin 9 as
PT marker to detect cancer metastasis for diagnosis, cancer prevention and
PT treatment.
XX
XX Disclosure; Page 63-64; 68pp; Japanese.

PS The specification describes an agent for detecting the ability of cancers
XX to metastasize. This agent comprises anti-galectin 9 antibody as the
CC active ingredient. The agents and method are for or detecting ability of
CC cancer to metastasize in cancer cells, which are useful in the diagnosis,
CC prevention and treatment of cancer. The cancer includes epithelial
CC malignant tumours (tumourising or non-tumourising) in organs, tissues or
CC blood. Such cancer can be 1 of the not less than 31 specifically claimed,
CC e.g. skin cancer (including melanoma), breast cancer, ovarian cancer,
CC uterus cancer, malignant tumour of the testis, prostate cancer, bladder
CC cancer, kidney cancer, thyroid cancer, cancer of throat and larynx, colon
CC tongue cancer, upper jaw cancer, esophageal cancer, stomach cancer, colon
CC and rectum cancer, lung and bronchus cancer, liver cancer (including
CC hepatocarcinoma and intrahepatic biliary cancer), extrahepatic biliary
CC duct and gall-bladder cancer, pancreatic cancer, leukemia, malignant
CC lymphoma, liposarcoma and glioma. The cancer cells are particularly
CC breast cancer cells or melanoma cells. The present sequence represents a
CC human protein, which is used in the course of the invention
XX
SQ Sequence 311 AA;

Query Match 98.4%; Score 306; DB 5; Length 311;
Best Local Similarity 100.0%; Pred. No. 4.6e-300; Indels 0; Gaps 0;
Matches 306; Conservative 0; Mismatches 0;

QY 6 SQAPYLSPAVPFSGTTQGGLODGLQITVNGTVLSSGTRFAVNFOTGSGNDIAFHNPR 65
DB 6 SQAPYLSPAVPFSGTTQGGLODGLQITVNGTVLSSGTRFAVNFOTGSGNDIAFHNPR 65
QY 66 FEDGGYVVCNTRQNSWGPEERKTHMPFQKGMPPFDLCFLVQSSDFKVMVNGILFVQYFHR 125
DB 66 FEDGGYVVCNTRQNSWGPEERKTHMPFQKGMPPFDLCFLVQSSDFKVMVNGILFVQYFHR 125
QY 126 VPFRVDTISVNGSVQLSYISFQTVIHTVQSAFGQMFSTPAIPPMYPHPAYPMEFIT 185
DB 126 VPFRVDTISVNGSVQLSYISFQTVIHTVQSAFGQMFSTPAIPPMYPHPAYPMEFIT 185
QY 186 TILGLYPSKILLSGTVLPFAORPHINLCGNHIAFHLNPRFDENAVVRNTQIDNSWGS 245
DB 186 TILGLYPSKILLSGTVLPFAORPHINLCGNHIAFHLNPRFDENAVVRNTQIDNSWGS 245
QY 246 EERSLPKMPFVRGQSFVWILCEAHCLKVAVDGQHLFEYHRLNLPINRLEVGDDIQ 305
DB 246 EERSLPKMPFVRGQSFVWILCEAHCLKVAVDGQHLFEYHRLNLPINRLEVGDDIQ 305
QY 306 LTHVQT 311
DB 306 LTHVQT 311

RESULT 3
ADP81097
ID ADP81097 standard; protein; 233 AA.

XX
AC ADP81097;
XX
DT 09-SEP-2004 (first entry)
XX
XX Protein of human ovarian specific gene, SEQ ID No 131.
DE
XX normal; neoplastic; ovarian; ovarian specific nucleic acid; OSNA;
KW metastatic; cancer; vaccine; cytostatic; human.

XX OS Homo sapiens.
 XX PN WO2004053079-A2.
 XX PD 24-JUN-2004.
 XX PF 08-DEC-2003; 2003WO-US038855.
 XX PR 06-DEC-2002; 2002US-0431301P.
 XX PR 06-DEC-2002; 2002US-0431321P.
 XX PR 30-JUN-2003; 2003US-0484584P.
 XX PR 07-NOV-2003; 2003US-0518607P.
 XX PA (DIAD-) DIADEXUS INC.
 XX PI Macina RA, Turner LR, Sun Y, Liu S, Chen H;
 XX WPI; 2004-468850/44.
 XX N-PSDB; ADP80968.
 XX New ovarian specific nucleic acid molecules and polypeptides useful for
 PT diagnosing, preventing or treating ovarian cancer, for producing
 PT transgenic animals or cells, or for research purposes.
 XX Claim 12; SEQ ID NO 131; 754pp; English.
 XX The invention relates to novel isolated nucleic acid molecules and
 CC polypeptides present in normal and neoplastic ovarian cells. These
 CC comprise a nucleic acid sequence encoding any of the 167 amino acid
 CC sequences (e.g. 438, 237 or 233 amino acids) fully defined in the
 CC specification (SEQ. ID NOS: ADP81095 to ADP81261) and comprises any of
 CC the 128 nucleotide sequences (e.g. 4798, 1494 or 1691 bp) fully defined
 CC in the specification (SEQ. ID NOS: ADP80967 to ADP81094). The invention
 CC further comprises: a method for determining the presence of a ovarian
 CC specific nucleic acid (OSNA) in a sample; a vector comprising the above
 CC nucleic acid molecule; a host cell comprising the vector; a method for
 CC producing a polypeptide encoded by the above nucleic acid molecule; a
 CC polypeptide encoded by the nucleic acid molecule cited above; an antibody
 CC or its fragment that specifically binds to the above polypeptide; a
 CC method for determining the presence of an ovarian specific protein in a
 CC sample; a method for diagnosing or monitoring the presence and metastases
 CC of ovarian cancer in a patient; a kit for detecting a risk of cancer or
 CC presence of cancer in a patient; the kit comprising a means for
 CC determining the presence of the above nucleic acid molecule or
 CC polypeptide; a method of treating a patient with ovarian cancer; and a
 CC vaccine comprising the above polypeptide or nucleic acid encoding the
 CC polypeptide. The isolated nucleic acid molecules and polypeptides have
 CC cytosstatic activity. The isolated polypeptides may be used to create a
 CC vaccine. The isolated nucleic acid molecules and polypeptides can be used
 CC for diagnosing or monitoring the presence and metastases of ovarian
 CC cancer and treating ovarian cancer. This sequence represents the protein
 CC of an ovarian specific gene of the invention.
 XX SQ Sequence 233 AA;
 Query Match 52.4%; Score 163; DB 8; Length 233;
 Best Local Similarity 100.0%; Pred. No. 8.7e-156;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 149 TOTVIHTVQSAPGQMFSTPAIPPMYHPAPMPFITTILGGLYPSKILLSGTVLPSAQ 208
 DB 71 TOTVIHTVQSAPGQMFSTPAIPPMYHPAPMPFITTILGGLYPSKILLSGTVLPSAQ 130
 QY 209 RFHINLCSGNHIAFLNPRFDENAVVRTQIDNSWGSEERSLPRKMPFVRGQSFVWLIC 268
 DB 131 RFHINLCSGNHIAFLNPRFDENAVVRTQIDNSWGSEERSLPRKMPFVRGQSFVWLIC 190
 QY 269 EAHCLKVAVDQGHLEFYHYHRLNLPNTINRLEVGDDIQLTHVQT 311
 DB 191 EAHCLKVAVDQGHLEFYHYHRLNLPNTINRLEVGDDIQLTHVQT 233

RESULT 4
 AAY56802 standard; protein; 323 AA.
 AAY56802;
 27-MAR-2000 (first entry)
 Human eosinophil chemotactic factor (ealelectin).
 Eosinophil chemotactic factor; galectin; chemotaxis inhibitor;
 inflammatory disorder; eosinophil; allergic disease; asthma; human;
 allergic rhinitis; atopic dermatitis; ealelectin; galectin.
 Homo sapiens.
 WO9962556-A1.
 09-DEC-1999.
 02-JUN-1999; 99WO-JP002952.
 03-JUN-1998; 98JP-00170698.
 (EPEF-) EFFECTOR CELL INST.
 Kanegasaki S, Matsumoto R, Hirashima M;
 WPI; 2000-086860/07.
 N-PSDB; AAZ46748.
 Ealelectin and other galectins as eosinophil chemotaxis promoters for
 screening potential inhibitors of this effect.
 Disclosure; Page 35-39; 49pp; Japanese.
 The invention provides compositions for increasing the chemotacticity of
 eosinophils that contain as active component a galectin. Chemotaxis
 inhibitors identified by the screening are used as agents for the
 treatment and prevention of inflammatory disorders caused by the increase
 of eosinophil content in affected tissues, such as allergic diseases
 including bronchial asthma, allergic rhinitis and atopic dermatitis. The
 present sequence represents a human eosinophil chemotactic factor,
 ealelectin. Ealelectin belongs to the family of galectin and has eosinophil
 chemotactic activity
 SQ Sequence 323 AA;
 Query Match 52.4%; Score 163; DB 3; Length 323;
 Best Local Similarity 100.0%; Pred. No. 1.2e-155;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 149 TOTVIHTVQSAPGQMFSTPAIPPMYHPAPMPFITTILGGLYPSKILLSGTVLPSAQ 208
 DB 161 TOTVIHTVQSAPGQMFSTPAIPPMYHPAPMPFITTILGGLYPSKILLSGTVLPSAQ 220
 QY 209 RFHINLCSGNHIAFLNPRFDENAVVRTQIDNSWGSEERSLPRKMPFVRGQSFVWLIC 268
 DB 221 RFHINLCSGNHIAFLNPRFDENAVVRTQIDNSWGSEERSLPRKMPFVRGQSFVWLIC 280
 QY 269 EAHCLKVAVDQGHLEFYHYHRLNLPNTINRLEVGDDIQLTHVQT 311
 DB 281 EAHCLKVAVDQGHLEFYHYHRLNLPNTINRLEVGDDIQLTHVQT 323
 RESULT 5
 ABB77853 standard; protein; 323 AA.
 ABB77853;
 27-SEP-2002 (first entry)

DE	Amino acid sequence of a human protein.	AC	ABP61494;
XX		XX	
XX	Cancer; galectin 9; antibody; skin cancer; melanoma; breast cancer;	XX	
KW	ovarian cancer; uterus cancer; tumor; prostate cancer; bladder cancer;	XX	
KW	kidney cancer; thyroid cancer; throat cancer; tongue cancer;	DE	30-SEP-2002 (first entry)
KW	upper jaw cancer; esophageal cancer; stomach cancer; colon cancer;	XX	Human NF-kB activating protein SEQ ID NO 141.
KW	lung cancer; liver cancer; gall-bladder cancer; pancreatic cancer;	KW	Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;
KW	leukemia; liposarcoma; glioma.	KW	immunomodulator; cytostatic; antiinfective; osteopathic; nootropic;
XX		KW	neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
OS	Homo sapiens.	KW	bone disease; AIDS; neurodegenerative disease; ischaemic disorder.
XX		XX	
XX	WO200237114-A1.	OS	Homo sapiens.
XX		XX	
XX	10-MAY-2002.	PN	WO200253737-A1.
XX		XX	
XX	31-OCT-2001; 2001WO-JP009561.	XX	11-JUL-2002.
XX		XX	
XX	01-NOV-2000; 2000JP-00335077.	XX	
XX		XX	25-DEC-2001; 2001WO-JP011389.
XX	(GALP-) GALPHARVA CO LTD.	XX	
XX	Hirashima M, Yamauchi A, Kageshita T, Nakamura T, Nishi N;	XX	28-DEC-2000; 2000JP-00402288.
XX		PR	26-MAR-2001; 2001JP-00089912.
XX	WPI; 2002-519265/55.	PR	24-AUG-2001; 2001JP-00254018.
XX		XX	
XX	Metastasis mechanism-based agents (anti-galectin 9 antibody) for	PA	(ASAH) ASAHI KASEI KOGYO KK.
PT	detecting ability of cancer to metastasize in cells, uses galectin 9 as	XX	
PT	marker to detect cancer metastasis for diagnosis, cancer prevention and	PI	Matsuda A, Honda G, Muramatsu S, Nagano Y;
PT	treatment.	XX	
XX		DR	WPI; 2002-583617/62.
XX		DR	N-PSDB; ABQ91982.
XX		XX	
PS	Example 5; Page 61-63; 68pp; Japanese.	XX	
XX		PT	NF-approximatelykB activating gene and expressed protein, applicable in
CC	The specification describes an agent for detecting the ability of cancers	PT	diagnosis and screening inhibitors or promoters to control excessive
CC	to metastasize. This agent comprises anti-galectin 9 antibody as the	PT	activation or inhibition for treating e.g. inflammations, autoimmune
CC	active ingredient. The agents and method are for or detecting ability of	PT	diseases and cancer.
CC	cancer to metastasize in cancer cells, which are useful in the diagnosis,	XX	
CC	prevention and treatment of cancer. The cancer includes epithelial	PS	Claim 1; Page 613-615; 841pp; Japanese.
CC	malignant tumours (tumourising or non-tumourising) in organs, tissues or	XX	
CC	blood. Such cancer can be 1 of the not less than 31 specifically claimed,	CC	The invention relates to a purified protein (I), comprising one of 90
CC	e.g. skin cancer (including melanoma), breast cancer, ovarian cancer,	CC	fully defined sequences (ABP61424-ABP61513) or a protein based on any of
CC	uterus cancer, malignant tumour of the testis, prostate cancer, bladder	CC	the sequences but with some amino acids deleted, substituted or added and
CC	cancer, kidney cancer, thyroid cancer, cancer of throat and larynx,	CC	with a NF-kB (nuclear factor kappa B) activating effect. The protein and
CC	tongue cancer, upper jaw cancer, esophageal cancer, stomach cancer, colon	CC	encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening
CC	and rectum cancer, lung and bronchus cancer, liver cancer (including	CC	inhibitors or promoters to control excessive activation or inhibition and
CC	hepatocarcinoma and intrahepatic biliary cancer), extrahepatic biliary	CC	for treating e.g. inflammations, autoimmune diseases, cancers,
CC	duct and gall-bladder cancer, pancreatic cancer, leukemia, malignant	CC	infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
CC	lymphoma, liposarcoma and glioma. The cancer cells are particularly	CC	disorders
CC	breast cancer cells or melanoma cells. The present sequence represents a	XX	
CC	human protein, which is used in the course of the invention	XX	
XX		SQ	Sequence 323 AA;
XX			
		Query Match	52.4%; Score 163; DB 5; Length 323;
		Best Local Similarity	100.0%; Pred. No. 1.2e-155;
		Matches 163; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	149 TQTVIHTVQSAPGQMFSTPAIPMMYPHPAYPMPFITITLGGLYPSKILLSGTVLPSAQ 208		
Db	161 TQTVIHTVQSAPGQMFSTPAIPMMYPHPAYPMPFITITLGGLYPSKILLSGTVLPSAQ 220		
Qy	209 RFHNLCSGNHIAFLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFVWILC 268		
Db	221 RFHNLCSGNHIAFLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFVWILC 280		
Qy	269 EAHCLKVAVDQQLHFEYTHRLNLPNTINRLEVGGDIQLTHVQT 311		
Db	281 EAHCLKVAVDQQLHFEYTHRLNLPNTINRLEVGGDIQLTHVQT 323		
		RESULT 7	
		ADQ66730	
		ID	ADQ66730 standard; protein; 323 AA.
		XX	
		AC	ADQ66730;
		XX	
		DT	07-OCT-2004 (first entry)

XX Novel human protein sequence #1703.
 DE
 XX
 KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
 KW gene therapy; diagnostic marker; morbid state; osteoporosis;
 KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
 KW cancer.
 XX
 OS Homo sapiens.
 OS
 PN EP1440981-A2.
 XX
 PD 28-JUL-2004.
 XX
 PP 21-JAN-2004; 2004EP-00001196.
 XX
 PR 21-JAN-2003; 2003JP-00102206.
 PR 09-MAY-2003; 2003JP-00131392.
 XX
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 PA
 XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 XX Yamamoto J, Isono Y, Nagai K, Irie R;
 PI
 PI WPI; 2004-535376/52.
 DR N-PSDB; ADQ64542.
 DR
 XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 XX
 PS Claim 1; SEQ ID NO 3891; 2449pp; English.
 XX
 CC The invention relates to 2495 novel polynucleotides (I) and their encoded
 CC polypeptides, sequences hybridizing to these nucleotides, sequences
 CC encoding partial polypeptides and sequences having 70% or 90% identity to
 CC the nucleotide and protein sequences. The nucleotides and polypeptides
 CC are useful as diagnostic markers or therapeutic target for the diseases
 CC or morbid states. They are also useful for treating osteoporosis,
 CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
 CC dementia and various cancers. This sequence corresponds to a protein
 CC sequence of the invention.
 XX
 SQ Sequence 323 AA;
 Query Match 52.4%; Score 163; DB 8; Length 323;
 Best Local Similarity 100.0%; Pred. No. 1.2e-155;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 149 TQTVHTVQSAPGQMFSTPAIPPMYPHPAYPMPFITTLGGLYPSKILLSGTVLPSAQ 208
 Db 161 TQTVHTVQSAPGQMFSTPAIPPMYPHPAYPMPFITTLGGLYPSKILLSGTVLPSAQ 220
 Qy 209 RFHNLCSGNHIAFLNPRFDENAVVRNTQIDNSGSEERSLPRKMPFVRGQSFVWILC 268
 Db 221 RFHNLCSGNHIAFLNPRFDENAVVRNTQIDNSGSEERSLPRKMPFVRGQSFVWILC 280
 Qy 269 EAHCLKVAVDQGHLEFYHRLNRLPTINRLEVGDDIQLTHVQT 311
 Db 281 EAHCLKVAVDQGHLEFYHRLNRLPTINRLEVGDDIQLTHVQT 323
 RESULT 8
 AAY06997
 ID AAY06997 standard; protein; 355 AA.
 XX
 AC AAY06997;
 XX
 XX 02-JUL-1999 (first entry)
 XX
 XX Galectin-9 protein sequence.
 XX
 KW Cancer associated antigen; diagnosis; research; treatment; human;
 KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;

KW prostate cancer.
 XX
 OS Homo sapiens.
 PN WO9904265-A2.
 XX
 PD 28-JAN-1999.
 XX
 PF 15-JUL-1998; 98WO-US014679.
 XX
 PR 17-JUL-1997; 97US-00896164.
 PR 10-OCT-1997; 97US-0061599P.
 PR 10-OCT-1997; 97US-0061765P.
 PR 10-OCT-1997; 97US-00948705.
 PR 11-OCT-1997; 97GB-00021697.
 PR 22-JUN-1998; 98US-00102322.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;
 PI O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;
 XX
 DR WPI; 1999-132448/11.
 DR N-PSDB; AAX40198.
 XX
 PT New isolated cancer associated nucleic acids and polypeptides - isolated
 PT using sera from cancer patients, used to develop products for the
 PT diagnosis, monitoring or treatment of cancers.
 XX
 PS Example 8; Page 779-780; 787pp; English.
 XX
 CC The invention relates to a method for diagnosing a disorder characterised
 CC by expression of a human cancer associated antigen precursor coded for by
 CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
 CC biological sample isolated from a subject with an agent that specifically
 CC binds to the NAM, an expression product or a fragment of an expression
 CC product complexed with an HLA molecule; and (b) determining the
 CC interaction between the agent and the NAM or the expression product as a
 CC determination of the disorder. The products and methods can be used in
 CC the diagnosis, monitoring, research, or treatment of conditions
 CC characterised by the expression of various cancer associated antigens.
 CC The invention provides nucleic acid sequences and encoded polypeptides
 CC which are cancer associated antigen precursors expressed in human breast
 CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
 CC lung cancer
 XX
 SQ Sequence 355 AA;
 Query Match 52.4%; Score 163; DB 2; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.3e-155;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 149 TQTVHTVQSAPGQMFSTPAIPPMYPHPAYPMPFITTLGGLYPSKILLSGTVLPSAQ 208
 Db 193 TQTVHTVQSAPGQMFSTPAIPPMYPHPAYPMPFITTLGGLYPSKILLSGTVLPSAQ 252
 Qy 209 RFHNLCSGNHIAFLNPRFDENAVVRNTQIDNSGSEERSLPRKMPFVRGQSFVWILC 268
 Db 253 RFHNLCSGNHIAFLNPRFDENAVVRNTQIDNSGSEERSLPRKMPFVRGQSFVWILC 312
 Qy 269 EAHCLKVAVDQGHLEFYHRLNRLPTINRLEVGDDIQLTHVQT 311
 Db 313 EAHCLKVAVDQGHLEFYHRLNRLPTINRLEVGDDIQLTHVQT 355
 RESULT 9
 AAW85664
 ID AAW85664 standard; protein; 355 AA.
 XX
 AC AAW85664;
 XX
 XX 19-JUL-1999 (first entry)
 DT
 XX

DE Galectin-9 like protein.
 XX Galectin-9; lectin; galactose; Hodgkin's disease; pharmaceutical;
 KW sugar chain; intercellular adhesion; cell proliferation.
 KW
 XX Homo sapiens.
 OS
 XX WO9910490-A1.
 PN
 XX
 XX 04-MAR-1999.
 PD
 XX
 XX 19-AUG-1998; 98WO-JP003670.
 XX
 XX 22-AUG-1997; 97JP-00226468.
 XX
 XX (SAGA) SAGAMI CHEM RES CENTRE.
 PA (PROT-) PROTEGENE INC.
 PA
 XX Kato S, Yamaguchi T, Sekine S, Kamata K;
 PI
 XX WPI; 1999-228913/19.
 DR
 DR N-PSDB; AAX08490, AAX08491.
 XX
 XX A new human protein having lactose binding properties.
 PT
 XX
 XX Claim 2; Page 55-57; 64pp; English.
 PS
 XX Galectins are the general term for animal lectins binding to galactose.
 CC
 CC Animal lectins exist in many sites such as the cytoplasm, the nucleus,
 CC the cell membrane etc. and are considered to be associated with cell
 CC proliferation. Galectin-9 has been identified as an antigenic protein
 CC reacting with an antibody contained in the serum of Hodgkin's disease and
 CC has a structure where two sugar chain-binding domains are connected by a
 CC linker peptide. The true role of galectin-9 in the body has not been
 CC completely identified but is thought to be involved in intercellular
 CC adhesion. The human galectin-9 like protein coding sequences are
 CC characterised by containing the sequence described in AAX08489. The
 CC protein can be used as pharmaceuticals or reagents for sugar chain
 CC research. The cDNA is used as a probe for gene diagnosis and for gene
 CC therapy
 XX
 XX SQ Sequence 355 AA;
 Query Match 52.4%; Score 163; DB 2; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.3e-155;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 149 TQTVIHTVQSAPGQMFSTPAIPPMYPHPAYPMPFITITLGGLYPSKSIILSGTVLPQAQ 208
 DB 193 TQTVIHTVQSAPGQMFSTPAIPPMYPHPAYPMPFITITLGGLYPSKSIILSGTVLPQAQ 252
 QY 209 RFHNLCSGNHIAFLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFVWILC 268
 DB 253 RFHNLCSGNHIAFLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFVWILC 312
 QY 269 EAHCLKVAVDQHLFEYFHYHRLNRLPTNRLNLEVGDIQLTHVQT 311
 DB 313 EAHCLKVAVDQHLFEYFHYHRLNRLPTNRLNLEVGDIQLTHVQT 355
 RESULT 10
 ABB77852
 ID ABB77852 standard; protein; 355 AA.
 XX
 XX ABB77852;
 AC
 XX
 XX 27-SEP-2002 (first entry)
 DT
 XX Amino acid sequence of a human protein.
 DE
 XX Cancer; galectin 9; antibody; skin cancer; melanoma; breast cancer;
 KW ovarian cancer; uterus cancer; tumour; prostate cancer; bladder cancer;
 KW kidney cancer; thyroid cancer; throat cancer; tongue cancer;

KW upper jaw cancer; esophageal cancer; stomach cancer; colon cancer;
 KW lung cancer; liver cancer; gall-bladder cancer; pancreatic cancer;
 KW leukemia; liposarcoma; glioma.
 XX
 OS Homo sapiens.
 XX
 XX WO200237114-A1.
 PN
 XX
 XX 10-MAY-2002.
 PD
 XX
 XX 31-OCT-2001; 2001WO-JP009561.
 PF
 XX
 XX 01-NOV-2000; 2000JP-00335077.
 PR
 XX
 XX (GALP-) GALPHARMA CO LTD.
 PA
 XX Hirashima M, Yamauchi A, Kageshita T, Nakamura T, Nishi N;
 PI
 XX WPI; 2002-519265/55.
 DR
 XX
 XX Metastasis mechanism-based agents (anti-galectin 9 antibody) for
 PT detecting ability of cancer to metastasize in cells, uses galectin 9 as
 PT marker to detect cancer metastasis for diagnosis, cancer prevention and
 PT treatment.
 XX
 XX Example 1; Page 60-61; 68pp; Japanese.
 PS
 XX The specification describes an agent for detecting the ability of cancers
 CC to metastasize. This agent comprises anti-galectin 9 antibody as the
 CC active ingredient. The agents and method are for or detecting ability of
 CC cancer to metastasize in cancer cells, which are useful in the diagnosis,
 CC prevention and treatment of cancer. The cancer includes epithelial
 CC malignant tumours (tumourising or non-tumourising) in organs, tissues or
 CC blood. Such cancer can be 1 of the not less than 31 specifically claimed,
 CC e.g. skin cancer (including melanoma), breast cancer, ovarian cancer,
 CC uterus cancer, malignant tumour of the testis, prostate cancer, bladder
 CC cancer, kidney cancer, thyroid cancer, cancer of throat and larynx,
 CC tongue cancer, upper jaw cancer, esophageal cancer, stomach cancer, colon
 CC and rectum cancer, lung and bronchus cancer, liver cancer (including
 CC hepatocarcinoma and intrahepatic biliary cancer), extrahepatic biliary
 CC duct and gall-bladder cancer, pancreatic cancer, leukemia, malignant
 CC lymphoma, liposarcoma and glioma. The cancer cells are particularly
 CC breast cancer cells or melanoma cells. The present sequence represents a
 CC human protein, which is used in the course of the invention
 XX
 XX SQ Sequence 355 AA;
 Query Match 52.4%; Score 163; DB 5; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.3e-155;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 149 TQTVIHTVQSAPGQMFSTPAIPPMYPHPAYPMPFITITLGGLYPSKSIILSGTVLPQAQ 208
 DB 193 TQTVIHTVQSAPGQMFSTPAIPPMYPHPAYPMPFITITLGGLYPSKSIILSGTVLPQAQ 252
 QY 209 RFHNLCSGNHIAFLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFVWILC 268
 DB 253 RFHNLCSGNHIAFLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFVWILC 312
 QY 269 EAHCLKVAVDQHLFEYFHYHRLNRLPTNRLNLEVGDIQLTHVQT 311
 DB 313 EAHCLKVAVDQHLFEYFHYHRLNRLPTNRLNLEVGDIQLTHVQT 355
 RESULT 11
 ADC53845
 ID ADC53845 standard; protein; 355 AA.
 XX
 XX ADC53845;
 AC
 XX
 XX 18-DEC-2003 (first entry)
 DT
 XX Human galectin 9 protein (long isoform).
 DE

XX KW galectin-9; nephritis; glomerular nephritis; antiinflammatory;
 KW glomerular infiltration; apoptosis; human.
 XX OS Homo sapiens.
 XX PN JP2002322082-A.
 XX PD 08-NOV-2002.
 XX PF 26-APR-2001; 2001JP-00129200.
 XX PR 26-APR-2001; 2001JP-00129200.
 XX PA (PROT-) PROTEGENE KK.
 XX DR WPI; 2003-367092/35.
 XX PT Agents for prevention and treatment of nephritis, comprise galectin-1,
 PT galectin-3, or galectin-9, by inhibition of intraglomerular infiltration
 PT of leukocytes, CD8 positive cells, and induction of apoptosis of CD8
 PT positive cells.
 XX PS Disclosure; SEQ ID NO 4; 31pp; Japanese.
 XX CC This invention relates to the use of novel mammal derived galectin-1
 CC (G1), -3 (G3) and -9 (G9) proteins as effective ingredients for
 CC prevention and treatment of nephritis. The invention discloses agents for
 CC prevention and treatment of nephritis, particularly glomerular nephritis
 CC and may have antiinflammatory activities. The method of the invention
 CC inhibits glomerular infiltration of leukocytes, CD8 positive cells and
 CC apoptosis of CD8 positive cells. The method and sequences of the
 CC invention may be used for prevention and treatment of nephritis,
 CC particularly glomerular nephritis including inhibition of glomerular
 CC infiltration of leukocytes, CD8 positive cells and apoptosis of CD8
 CC positive cells. The present sequence represents the human galectin 9
 CC protein (long isoform) used in the exemplification of the present
 CC invention.
 XX SQ Sequence 355 AA;
 Query Match 52.4%; Score 163; DB 7; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.3e-155;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 149 TQTVHTVQSAPGQMFSTPAIPPMYPHPAYPMPFITTLGLGYPSKILLSGTVLPQAQ 208
 DB 193 TQTVHTVQSAPGQMFSTPAIPPMYPHPAYPMPFITTLGLGYPSKILLSGTVLPQAQ 252
 QY 209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFVWILC 268
 DB 253 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFVWILC 312
 QY 269 EAHCLKVAVDQGHLPFYHYHRLNRLPTINRLEVGGDIQLTHVQT 311
 DB 313 EAHCLKVAVDQGHLPFYHYHRLNRLPTINRLEVGGDIQLTHVQT 355
 RESULT 12
 ADE62929
 ID ADE62929 standard; protein; 355 AA.
 XX AC ADE62929;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human Protein O00182, SEQ ID NO 8863.
 XX KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX OS Homo sapiens.

XX WO2003016475-A2.
 XX PD 27-FEB-2003.
 XX PF 14-AUG-2002; 2002WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 XX PR 01-NOV-2001; 2001US-0346382P.
 XX PR 26-NOV-2001; 2001US-0333347P.
 XX PA (GEHO) GEN HOSPITAL CORP.
 XX PA (PARB) BAYER AG.
 XX PI Woolf C, D'urso D, Befort K, Costigan M;
 XX DR WPI; 2003-268312/26.
 XX DR GENBANK; O00182.
 XX PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX PS Claim 1; Page; 1017pp; English.
 XX CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 355 AA;
 Query Match 52.4%; Score 163; DB 7; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.3e-155;
 Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 149 TQTVHTVQSAPGQMFSTPAIPPMYPHPAYPMPFITTLGLGYPSKILLSGTVLPQAQ 208
 DB 193 TQTVHTVQSAPGQMFSTPAIPPMYPHPAYPMPFITTLGLGYPSKILLSGTVLPQAQ 252
 QY 209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFVWILC 268
 DB 253 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFVWILC 312
 QY 269 EAHCLKVAVDQGHLPFYHYHRLNRLPTINRLEVGGDIQLTHVQT 311
 DB 313 EAHCLKVAVDQGHLPFYHYHRLNRLPTINRLEVGGDIQLTHVQT 355
 RESULT 13
 ADD48101

AD48101 standard; protein; 355 AA.	Qy	149	TQTVIHTVQSAPGQMFSTPAIPPMYPHPAYPMPFITTLGGLYPSKILLSGTVLPSAQ	208
ADD48101;	Db	193	TQTVIHTVQSAPGQMFSTPAIPPMYPHPAYPMPFITTLGGLYPSKILLSGTVLPSAQ	252
02-DEC-2004 (revised)	Qy	209	RHINILCSGNHIAFLNPRDENAVRNTQIDNSWSEERSLPRKMPFVVGQSFVWILC	268
29-JAN-2004 (first entry)	Db	253	RHINILCSGNHIAFLNPRDENAVRNTQIDNSWSEERSLPRKMPFVVGQSFVWILC	312
Human Protein O00182, SEQ ID NO 13799.	Qy	269	EAHCLKVAVDGOHLFEYHRLRLPTINRLEVGGDIQLTHVQT	311
Human; pain; neuronal tissue; gene therapy;	Db	313	EAHCLKVAVDGOHLFEYHRLRLPTINRLEVGGDIQLTHVQT	355
spinal segmental nerve injury; chronic constriction injury; CCI;				
spared nerve injury; SNI; Chung.				
Homo sapiens.				
Unidentified.				
WO2003016475-A2.				
27-FEB-2003.				
14-AUG-2002; 2002WO-US025765.				
14-AUG-2001; 2001US-0312147P.				
01-NOV-2001; 2001US-0346382P.				
26-NOV-2001; 2001US-0333347P.				
(GEHO) GEN HOSPITAL CORP.				
(FARB) BAYER AG.				
Woolf C, D'urso D, Befort K, Costigan M;				
WPI; 2003-268312/26.				
GENBANK; O00182.				
New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.				
Example 1; Page; 1017pp; English.				
The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (described in Table 3 of the specification) which is differentially expressed during pain.				
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.				
Sequence 355 AA;	Qy	149	TQTVIHTVQSAPGQMFSTPAIPPMYPHPAYPMPFITTLGGLYPSKILLSGTVLPSAQ	208
Query Match				
Best Local Similarity				
Matches 163; Conservative				
52.4%; Score 163; DB 7; Length 355;				
100.0%; Pred. No. 1.3e-155;				
0; Mismatches 0; Indels 0; Gaps 0;				

Db 193 TOTVIHTVQSAPGQMFSTPAIPPMYHPAYPMBPITITILGGLYPSKILLSGTVLPSAQ 252
Qy 209 RFHINLCSGNHIAFLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRQGSFVWILC 268
Db 253 RFHINLCSGNHIAFLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRQGSFVWILC 312
Qy 269 EAHCLKVAVDQOHLFEYHYHRLRNLPTINRLEVGGDIQLTHVQT 311
Db 313 EAHCLKVAVDQOHLFEYHYHRLRNLPTINRLEVGGDIQLTHVQT 355

RESULT 15

AAE13847
ID AAE13847 standard; protein; 378 AA.

XX
AC AAE13847;

XX
DT 26-FEB-2002 (first entry)

XX
XX Human lung tumour-specific protein 21871.

XX
XX Human; lung tumour protein; immunostimulant; cytostatic; gene therapy;
KW antisense-therapy; vaccine; immune response; lung cancer; 21871.

XX
OS Homo sapiens.

XX
XX Key Location/Qualifiers

XX
FH Misc-difference 182..183

XX
FT /note= "Encoded by TTTCC"

XX
XX WO200172295-A2.

XX
XX 04-OCT-2001.

XX
XX 28-MAR-2001; 2001WO-US009991.

XX
XX 29-MAR-2000; 2000US-00538037.

XX
XX 05-JUN-2000; 2000US-00588937.

XX
XX 18-AUG-2000; 2000US-00640878.

XX
XX 22-SEP-2000; 2000US-0234517P.

XX
XX 01-NOV-2000; 2000US-00704512.

XX
XX 14-DEC-2000; 2000US-00738973.

XX
XX (CORI-) CORIXA CORP.

XX
XX Reed SG, Lodes MJ, Mohamath R, Secrist H, Benson DR, Indirias CY;
PI Henderson RA, Fling SP, Algate PA, Elliot M, Mammion J, Kalos MD;

XX
XX WPI; 2001-639201/73.

XX
XX N-PSDB; AAD23459.

XX
XX New human lung-specific polynucleotides and polypeptides for the
PT diagnosis and treatment of disease e.g. lung cancer.

XX
XX Disclosure; Page 331; 378pp; English.

XX
XX The invention relates to isolated lung tumour-specific proteins and their
CC corresponding cDNA molecules. Lung tumour-specific proteins and their
CC antigen-presenting cells are useful for stimulating and/or expanding T
CC cells specific for a tumour protein, and for inhibiting the development
CC of cancer. The invention also relates to a composition useful for
CC stimulating an immune response, and for treating cancer. The lung tumour
CC specific oligonucleotide is useful in gene therapy and for diagnosis,
CC detection and treatment of lung cancer. The present sequence is human
XX lung tumour-specific protein

XX
SQ Sequence 378 AA;

Query Match 52.4%; Score 163; DB 4; Length 378;

Best Local Similarity 100.0%; Pred. No. 1.4e-155;

Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TOTVIHTVQSAPGQMFSTPAIPPMYHPAYPMBPITITILGGLYPSKILLSGTVLPSAQ 208
Db 216 TOTVIHTVQSAPGQMFSTPAIPPMYHPAYPMBPITITILGGLYPSKILLSGTVLPSAQ 275
Qy 209 RFHINLCSGNHIAFLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRQGSFVWILC 268
Db 276 RFHINLCSGNHIAFLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRQGSFVWILC 335
Qy 269 EAHCLKVAVDQOHLFEYHYHRLRNLPTINRLEVGGDIQLTHVQT 311
Db 336 EAHCLKVAVDQOHLFEYHYHRLRNLPTINRLEVGGDIQLTHVQT 378

Search completed: July 13, 2005, 07:50:31

Job time : 167 secs

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OM protein - protein search, using sw model

Run on: July 13, 2005, 07:46:47 ; Search time 40 Seconds
(without alignments)
748.085 Million cell updates/sec

Title: US-09-263-689-4
Perfect score: 311
Sequence: 1 MAFSGQAPYLSPAVPFGT.....LPTINRLEVGDIQLTHVQT 311

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	6.4	145	2 A55932	galectin-5 - rat
2	12	3.9	245	2 A54909	carbohydrate-bindi
3	12	3.9	262	2 A54889	IGG-binding protei
4	10	3.2	324	2 A46631	lactose-binding le
5	8	2.6	139	2 S08576	lectin - mouse (fr
6	8	2.6	242	2 JC4300	galectin-3 - rabbi
7	8	2.6	250	2 A35820	galectin 3 - human
8	8	2.6	264	2 A28651	galactose-specific
9	8	2.6	264	2 A45983	lactose-binding le
10	8	2.6	294	2 A49688	lactose-binding le
11	8	2.6	316	2 A55975	galectin-8 - rat
12	8	2.6	317	2 JC6147	prostate carcinoma
13	8	2.6	323	2 A55664	lectin L-36 - pig
14	8	2.6	881	2 AD2580	two component sens
15	8	2.6	881	2 C97362	protein sensor pro
16	8	2.6	1433	2 S54587	CAR8 protein - yea
17	7	2.3	161	2 S44757	ribosomal protein
18	7	2.3	169	1 S23478	probable benzoate
19	7	2.3	214	2 S21969	19K zein precursor
20	7	2.3	228	2 G95935	conserved hypothet
21	7	2.3	230	1 Z1ZMA2	19K zein precursor
22	7	2.3	233	2 S47266	zein Zdl, 19K - ma
23	7	2.3	233	2 S15656	zein, 19K - maize
24	7	2.3	233	2 S47265	zein Zdl, 19K - ma
25	7	2.3	234	1 Z1ZM3	19K zein precursor
26	7	2.3	235	2 S15655	zein, 19K - maize
27	7	2.3	269	2 G75148	hypothetical prote
28	7	2.3	279	2 T37216	beta-galactoside-b
29	7	2.3	285	2 T26325	hypothetical prote

30	7	2.3	296	2 A64110	cell division inhi
31	7	2.3	307	2 A28771	reaction center pr
32	7	2.3	308	1 WNRFS	reaction center pr
33	7	2.3	308	2 T50761	reaction center pr
34	7	2.3	308	2 S24213	hypothetical prote
35	7	2.3	310	2 AD2557	hypothetical prote
36	7	2.3	325	2 T50890	photosynthetic rea
37	7	2.3	325	2 F49964	photosynthetic rea
38	7	2.3	325	2 D95897	probable cellulase
39	7	2.3	327	2 G83551	hypothetical prote
40	7	2.3	331	2 S44962	lmb2 protein - Str
41	7	2.3	332	2 C96000	probable C4-dicarb
42	7	2.3	335	2 A13111	hypothetical prote
43	7	2.3	335	2 D98175	hypothetical prote
44	7	2.3	344	2 T26901	hypothetical prote
45	7	2.3	345	2 C55741	thymopoietin gamma

ALIGNMENTS

RESULT 1

A55932
N;Alternate names: beta-galactoside binding lectin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: A55932; PX0077
R;Gitt, M.A.; Wiser, M.F.; Leffler, H.; Herrmann, J.; Xia, Y.R.; Massa, S.M.; Cooper, D.
J. Biol. Chem. 270, 5032-5038, 1995
A;Title: Sequence and mapping of galectin-5, a beta-galactoside-binding lectin, found in
A;Reference number: A55932; MUID:95197487; PMID:7890611
A;Accession: A55932
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-145 <GIT>
A;Cross-references: UNIPROT:P47967; GB:L36862; NID:G727175; PIDN:AAC42050.1; PID:G727176
J;Jung, S.K.; Fujimoto, D.
J. Biochem. 116, 547-553, 1994
A;Title: A novel beta-galactoside-binding lectin in adult rat kidney.
A;Reference number: PX0077; MUID:95155264; PMID:7852273
A;Accession: PX0077
A;Molecule type: protein
A;Residues: 7,'P',9-10,'T',12-19,'X',21-25;30-42;109-111,'N',113,'H',115,'VS',118-123,'K'
A;Experimental source: kidney
C;Comment: This protein exhibits activity to various saccharides and binds to Engelbreth
C;Genetics:
A;Gene: LGALS5
C;Superfamily: beta-galactoside-binding lectin
C;Keywords: acetylated amino end; lectin; monomer
F;2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

Query Match 6.4%; Score 20; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 3.7e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	220	IAFHLPFRFDENAVVRNTQI	239
Db	54	IAFHLPFRFDENAVVRNTQI	73

RESULT 2

A54909
N;Alternate names: S-type animal lectin CBP30
C;Species: Criceinae gen. sp. (hamster)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 20-Aug-1999
C;Accession: A54909
R;Mehul, B.; Bawumia, S.; Martin, S.R.; Hughes, R.C.
J. Biol. Chem. 269, 18250-18258, 1994
A;Title: Structure of baby hamster kidney carbohydrate-binding protein CBP30, an S-type
A;Reference number: A54909; MUID:94299546; PMID:8027086
A;Accession: A54909

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-245 <HEH>
A;Cross-references: GB:X78879; NID:G535082; PIDN:CAAS4479.1; PID:G535083
C;Superfamily: beta-galactoside-binding lectin
C;Keywords: lectin

Query Match 3.9%; Score 12; DB 2; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.00017; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 GNDIAFHFNPRF 66
Db 147 GNDIAFHFNPRF 158
|||||

RESULT 3
A54889
IGB-binding protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 09-Jul-2004
C;Accession: A54889; A23148
R;Albrandt, K.; Orida, N.K.; Liu, F.T.
Proc. Natl. Acad. Sci. U.S.A. 84, 6859-6863, 1987
A;Title: An IGE-binding protein with a distinctive repetitive sequence and homology with A;Reference number: A54889; MUID:88016189; PMID:2958848
A;Accession: A54889
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-262 <ALB>
A;Cross-references: UNIPROT:P08699; GB:J02962; NID:G2031173; PIDN:AAA40828.1; PID:G203174
R;Liu, F.T.; Albrandt, K.; Mendel, E.; Kulczycki Jr., A.; Orida, N.K.
Proc. Natl. Acad. Sci. U.S.A. 82, 4100-4104, 1985
A;Title: Identification of an IGE-binding protein by molecular cloning.
A;Reference number: A23148; MUID:85216641; PMID:3858867
A;Accession: A23148
A;Molecule type: mRNA
A;Residues: 125-262 <LIU>
A;Cross-references: GB:M13697; NID:G204727; PIDN:AAA41378.1; PID:G204728
C;Superfamily: beta-galactoside-binding lectin
C;Keywords: lectin; phosphoprotein

Query Match 3.9%; Score 12; DB 2; Length 262;
Best Local Similarity 100.0%; Pred. No. 0.00018; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 GNDIAFHFNPRF 66
Db 164 GNDIAFHFNPRF 175
|||||

RESULT 4
A46631
lactose-binding lectin L-36 - rat
N;Alternate names: galectin-4
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Sep-1993 #sequence_revision 19-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46631; S63096
R;Oda, Y.; Herrmann, J.; Gitt, M.A.; Turck, C.W.; Burlingame, A.L.; Barondes, S.H.; Lefk J. Biol. Chem. 268, 5929-5939, 1993
A;Title: Soluble lactose-binding lectin from rat intestine with two different carbohydrate A;Reference number: A46631; MUID:93194902; PMID:8449956
A;Accession: A46631
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-324 <ODA>
A;Cross-references: UNIPROT:P38552; GB:M73553; NID:G294571; PIDN:AAA41505.1; PID:G294572
A;Experimental source: intestine
A;Note: sequence extracted from NCBI backbone (NCBIN:128409, NCBIP:128410)
R;Hardy, F.; Deviller, P.; Louisot, P.; Martin, A.
FEBS Lett. 359, 169-172, 1995
A;Title: Purification and characterization of the N-terminal domain of galectin-4 from A;Reference number: S69096; MUID:9517227; PMID:7867792

A;Accession: S69096
A;Molecule type: protein
A;Residues: 13-37;44-50,'E',52-66 <TAR>
C;Superfamily: lactose-binding lectin L-36
C;Keywords: lectin

Query Match 3.2%; Score 10; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 0.029; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 DIAFHFNPRF 66
Db 59 DIAFHFNPRF 68
|||||

RESULT 5
S08576
lectin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S08576
R;Raz, A.; Carmi, P.; Pazerini, G.
Cancer Res. 48, 645-649, 1988
A;Title: Expression of two different endogenous galactoside-binding lectins sharing sequ A;Reference number: S07162; MUID:88080093; PMID:3335026
A;Accession: S08576
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-139 <RAZ>
A;Cross-references: UNIPROT:Q61357
C;Superfamily: beta-galactoside-binding lectin

Query Match 2.6%; Score 8; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.8; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 AFHFNPRF 66
Db 72 AFHFNPRF 79
|||||

RESULT 6
JC4300
galectin-3 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4300
R;Gaudin, J.C.; Monsigny, M.; Legrand, A.
Gene 163, 249-252, 1995
A;Title: Cloning of the cDNA encoding rabbit galectin-3.
A;Reference number: JC4300; MUID:96011642; PMID:7590275
A;Accession: JC4300
A;Molecule type: mRNA
A;Residues: 1-242 <GAU>
A;Cross-references: UNIPROT:P47845; GB:U06470; NID:G606794; PIDN:AA48491.1; PID:G606795
A;Experimental source: vascular smooth muscle cells
A;Note: The authors translated the codon TTC for residue 155 as Leu
C;Comment: This protein has the functions on cell adhesion and proliferation. It is a su C;Genetics:
A;Gene: lgals3
C;Superfamily: beta-galactoside-binding lectin
C;Keywords: muscle

Query Match 2.6%; Score 8; DB 2; Length 242;
Best Local Similarity 100.0%; Pred. No. 2.9; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 AFHFNPRF 66
Db 148 AFHFNPRF 155
|||||

RESULT 7

A35820
 Galactin 3 - human
 N;Alternate names: CBP 35; epithelial-specific lectin 35; galactoside-binding lectin L-2
 C;Species: Homo sapiens (man)
 C;Date: 12-Oct-1990 #sequence revision 12-Oct-1990 #text_change 09-Jul-2004
 C;Accession: A35820; J00916; A47473; A36071; A49800
 R;Robertson, M.W.; Albrandt, K.; Keller, D.; Liu, F.T.
 Biochemistry 29, 8093-8100, 1990
 A;Title: Human IgG-binding protein: a soluble lectin exhibiting a highly conserved inter
 A;Reference number: A35820; MUID:91084480; PMID:2261464
 A;Accession: A35820
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-250 <ROS>
 A;Cross-references: UNIPROT:P17931; GB:M57710; NID:g179530; PIDN:AAA35607.1; PID:g179531
 R;Oda, Y.; Lefler, H.; Sakakura, Y.; Kasai, K.; Barondes, S.H.
 Gene 99, 279-283, 1991
 A;Title: Human breast carcinoma cDNA encoding a galactoside-binding lectin homologous to
 A;Reference number: J00916; MUID:91216471; PMID:2022338
 A;Accession: J00916
 A;Molecule type: mRNA
 A;Residues: 1-250 <ODA>
 A;Cross-references: GB:M36682; NID:g186921; PIDN:AAA36163.1; PID:g186922
 R;Lotz, M.M.; Andrews Jr., C.W.; Korzelius, C.A.; Lee, E.C.; Steele Jr., G.D.; Clarke, A.
 Proc. Natl. Acad. Sci. U.S.A. 90, 3466-3470, 1993
 A;Title: Decreased expression of Mac-2 (carbohydrate binding protein 35) and loss of its
 A;Reference number: A47473; MUID:93234518; PMID:7682704
 A;Accession: A47473
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-63, 'P', 65-97, 'T', 99-250 <LOT>
 A;Cross-references: GB:S59012; NID:g299601; PIDN:AAB26229.1; PID:g299602
 A;Experimental source: normal colonic mucosa, colon carcinoma, cell line clone A
 A;Note: sequence extracted from NCBI backbone (NCBIN:129689, NCBI:P129692)
 R;Cheravil, B.J.; Chaitovitz, S.; Wong, C.; Pillai, S.
 Proc. Natl. Acad. Sci. U.S.A. 87, 7324-7328, 1990
 A;Title: Molecular cloning of a human macrophage lectin specific for galactose.
 A;Reference number: A36071; MUID:90384999; PMID:2402511
 A;Accession: A36071
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-32, 'Q', 34, 'L', 37, 'RGFLSWGL', 46, 'RAGT', 51, 'R', 53-63, 'P', 65-87, 89-250 <CHE>
 A;Cross-references: GB:M35368; NID:g1196441
 A;Note: the sequence is revised in GenBank entry HUMMAC2, release 113.0, PIDN:AAA8086.1
 R;Raz, A.; Carmi, P.; Raz, T.; Hogan, V.; Mohamed, A.; Wolman, S.R.
 Cancer Res. 51, 2173-2178, 1991
 A;Title: Molecular cloning and chromosomal mapping of a human galactoside-binding protei
 A;Reference number: A49800; MUID:91183475; PMID:2009535
 A;Accession: A49800
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-32, 'Q', 34, 'LPGAYPGAYPACTPGLSWTAPPGATMHEVLIRSTCTWSLRTQ', 86-104, 'A', 106, 'M
 A;Cross-references: GB:M64303; NID:g413862
 A;Note: this translation is not annotated in GenBank entry HUMGALBIN, release 113.0
 C;Genetics:
 A;Gene: GDB:LGALS3; MAC-2; LGALS2
 A;Cross-references: GDB:127515; OMIM:137033
 A;Map position: lp13-1p13
 C;Superfamily: beta-galactoside-binding lectin
 C;Keywords: lectin; nucleus; phosphoprotein
 Query Match 2.6%; Score 8; DB 2; Length 250;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 59 AFHFNPRF 66
 Db 156 AFHFNPRF 163
 RESULT 8
 A28651
 galactose-specific lectin - mouse

N;Alternate names: carbohydrate-binding protein 35; IgE-binding protein; lectin L-34; Ma
 C;Species: Mus musculus (house mouse)
 C;Date: 28-Aug-1989 #sequence revision 10-Feb-1995 #text_change 09-Jul-2004
 C;Accession: S08537; A28651; A37385; A35185
 R;Cheravil, B.J.; Weiner, S.J.; Pillai, S.
 J. Exp. Med. 170, 1959-1972, 1989
 A;Title: The Mac-2 antigen is a galactose-specific lectin that binds IgE.
 A;Reference number: S08537; MUID:90063462; PMID:2584931
 A;Accession: S08537
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-264 <CHE>
 A;Cross-references: UNIPROT:P16110; EMBL:X16834; NID:g52986; PIDN:CAA34736.1; PID:g52987
 A;Note: this sequence was submitted to the EMBL Data Library, Oct-1989
 R;Jia, S.; Wang, J.L.
 J. Biol. Chem. 263, 6009-6011, 1988
 A;Title: Carbohydrate binding protein 35. Complementary DNA sequence reveals homology wi
 A;Reference number: A28651; MUID:98198129; PMID:3360772
 A;Accession: A28651
 A;Molecule type: mRNA
 A;Residues: 'R', 3-264 <JIA>
 A;Cross-references: EMBL:J03723
 R;Raz, A.; Pazerini, G.; Carmi, P.
 Cancer Res. 49, 3489-3493, 1989
 A;Title: Identification of the metastasis-associated, galactoside-binding lectin as a ch
 A;Reference number: A37385; MUID:9275058; PMID:2525069
 A;Accession: A37385
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-3, 'T', 5-91, 'ST', 94-109, 'SAP', 113-264 <RAZ>
 A;Cross-references: GB:I6074; NID:g52850; PIDN:CAA34206.1; PID:g52851
 A;Note: authors translated the codon GAA for residue 219 as Ala, GAC for residue 221 as
 R;Woo, H.J.; Shaw, L.M.; Messier, J.M.; Mercurio, A.M.
 J. Biol. Chem. 265, 7097-7099, 1990
 A;Title: The major non-integrin laminin binding protein of macrophages is identical to c
 A;Reference number: A35185; MUID:90236991; PMID:2332426
 A;Accession: A35185
 A;Molecule type: protein
 A;Residues: 159-163; 166-175; 214-226 <WOO>
 C;Superfamily: beta-galactoside-binding lectin
 C;Keywords: lectin; phosphoprotein
 Query Match 2.6%; Score 8; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 59 AFHFNPRF 66
 Db 170 AFHFNPRF 177
 RESULT 9
 A45983
 lactose-binding lectin Mac-2 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
 C;Accession: A45983
 R;Rosenberg, I.M.; Iyer, R.; Cheravil, B.; Chiodino, C.; Pillai, S.
 J. Biol. Chem. 268, 12393-12400, 1993
 A;Title: Structure of the murine Mac-2 gene. Splice variants encode proteins lacking fur
 A;Reference number: A45983; MUID:93286070; PMID:8509379
 A;Accession: A45983
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-264 <ROS>
 A;Cross-references: UNIPROT:Q8C253; GB:L08649
 C;Genetics:
 A;Introns: 6/3; 128/3; 158/2; 209/2; 213/3
 C;Superfamily: beta-galactoside-binding lectin
 Query Match 2.6%; Score 8; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 AFHFNPRF 66
 Db 170 AFHFNPRF 177

RESULT 10
 A49688
 lactose-binding lectin L-29 - dog
 C;Species: Canis lupus familiaris (dog)
 C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 24-Nov-1999
 C;Accession: A49688
 R;Hermann, J.; Turck, C.W.; Atchison, R.E.; Huflejt, M.E.; Poulter, L.; Gitt, M.A.; Bur
 J. Biol. Chem. 268, 26704-26711, 1993
 A;Title: Primary structure of the soluble lactose binding lectin L-29 from rat and dog a
 agenase.
 A;Reference number: A49688; MUID:94075368; PMID:8253805
 A;Accession: A49688
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-294 <HER>
 A;Cross-references: GB:L23429
 C;Superfamily: beta-galactoside-binding lectin
 C;Keywords: acetylated amino end
 F;1/Modified site: acetylated amino end (Ala) #status experimental

Query Match 2.6%; Score 8; DB 2; Length 294;
 Best Local Similarity 100.0%; Pred. No. 3.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 AFHFNPRF 66
 Db 200 AFHFNPRF 207

RESULT 11
 A55975
 galectin-8 - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
 C;Accession: A55975
 R;Hadari, Y.R.; Paz, K.; Dekel, R.; Mestrovic, T.; Accili, D.; Zick, Y.
 J. Biol. Chem. 270, 3447-3453, 1995
 A;Title: Galectin-8. A new rat lectin, related to galectin-4.
 A;Reference number: A55975; MUID:95155445; PMID:7852431
 A;Accession: A55975
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-316 <HAD>
 A;Cross-references: UNIPROT:Q62665; GB:U09824; NID:g717031; PIDN:AAA66359.1; PID:g717032
 C;Superfamily: lactose-binding lectin L-36

Query Match 2.6%; Score 8; DB 2; Length 316;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 AFHFNPRF 66
 Db 62 AFHFNPRF 69

RESULT 12
 JC6147
 prostate carcinoma tumor antigen 1 - human
 C;Species: Homo sapiens (man)
 C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 29-Sep-1999
 C;Accession: JC6147
 R;Su, Z.Z.; Lin, J.; Shen, R.; Fisher, P.E.; Goldstein, N.I.; Fisher, P.B.
 Proc. Natl. Acad. Sci. U.S.A. 93, 7252-7257, 1996
 A;Title: Surface-epitope masking and expression cloning identifies the human prostate ca
 A;Reference number: JC6147; MUID:96293510; PMID:8692978
 A;Accession: JC6147
 A;Molecule type: mRNA

A;Residues: 1-317 <SUA>
 A;Cross-references: GB:L78132; NID:g1932711; PIDN:AAB51605.1; PID:g1932712
 C;Comment: This protein is a therapeutic reagent for intervention in pervasive and fatal
 tein is a member of the galectin family.
 C;Superfamily: lactose-binding lectin L-36
 C;Keywords: tumor

Query Match 2.6%; Score 8; DB 2; Length 317;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 AFHFNPRF 66
 Db 63 AFHFNPRF 70

RESULT 13
 A55664
 lectin L-36 - pig
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
 C;Accession: A55664
 R;Chiu, M.L.; Parry, D.A.D.; Feldman, S.R.; Klapper, D.G.; O'Keefe, E.J.
 J. Biol. Chem. 269, 31770-31776, 1994
 A;Title: An adherens junction protein is a member of the family of lactose-binding lecti
 A;Reference number: A55664; MUID:95081129; PMID:7989350
 A;Accession: A55664
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-323 <CHI>
 A;Cross-references: UNIPROT:Q29058; GB:X79303; NID:g623345; PIDN:CAA55884.1; PID:g623346
 C;Superfamily: lactose-binding lectin L-36

Query Match 2.6%; Score 8; DB 2; Length 323;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 AFHFNPRF 66
 Db 61 AFHFNPRF 68

RESULT 14
 AD2580
 two component sensor kinase Atu0027 [imported] - Agrobacterium tumefaciens (strain C58, 1
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C;Accession: AD2580
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell
 i Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, 1
 ster, B.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: AD2580
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-881 <KUR>
 A;Cross-references: UNIPROT:Q8UJAI; GB:AE008688; PIDN:AAL41058.1; PID:g17738345; GSPDB:GN
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:

A;Gene: Atu0027
 A;Map position: circular chromosome

Query Match 2.6%; Score 8; DB 2; Length 881;
 Best Local Similarity 100.0%; Pred. No. 9.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 ILLSGTVL 204
 Db 69 ILLSGTVL 76

RESULT 15

C97362
protein sensor protein (AF042096) [imported] - Agrobacterium tumefaciens (strain C58, Ce
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97362
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C97362
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-881 <KUR>
A;Cross-references: UNIPROT:Q8UJ1; GB:AE007869; PIDN:AAK85852.1; PID:gl5154889; GSPDB:G
C;Genetics:
A;Gene: AGR_C_44
A;Map position: circular chromosome

Query Match 2.6%; Score 8; DB 2; Length 881;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 197 ILLSGTVL 204
|||
Db 69 ILLSGTVL 76

Search completed: July 13, 2005, 08:02:31
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